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Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	BD012071	RESULT 1
Kawai, Y . Fatty acid transfer protein, and a gene encoding the protein	Morikawa, N., Masuho, Y., Ota, T., Isogai, T., Nishikawa, T. and	1 (bases 1 to 2405)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens (human)	WO 0104301-A/1.	BD012071.1 GI:22092260	BD012071	Fatty acid transfer protein, and a gene encoding the protein.	BD012071 2405 bp DNA linear PAT 02-AUG-2002		

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541 CTGGGACCCGACGCGCACAGCGGCACAGCGGCACAGCGGACACGCTGCAGAAAGCGACACGCACACGCACAGCGACAGCAGCACAGCAG	421 GGCCCAGCAGCGCGCGCACACCTTTCTCATTCACGGCTCGCGCGCTTTAGCTACTC 480	O1 CTTTGCGGTGCGAGCTCTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCCTGGCCGCGGG 36	181 GATAGAGGAAGCGGGCTCCATGGCTGCCCTCCTGCTGCTGCTGCTGCTGCTGCTACC 240	61 GGGCGTGTGCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGC 120	y Match 100.0%; Score 2405; DB 6; Length 2405; Local Similarity 100.0%; Pred. No. 0; hes 2405; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 GCACTCCTCCCGGGTTTCTGCTCTCCGCCCGTGTGGAGTGGGCCTGGGTGGG	FH Key Location/Qualifiers FT CDS Location/Qualifiers 12405 Curce /organism="Homo sapiens" /mol_type="genomic_DNA" /db_xref="taxon:9606"	PD 18-JAN-2001 PF 07-JUL-2001 WO 2000JP004549 PF 08-JUL-1999 JP 99P 194179, 25-APR-2000 JP 00P 128993 PR 18-OCT-1999 US 60/159586 PI NORIYUKI MORIKAWA, YASUHIKO MASUHO, TOSHIO OTA, TAKAO ISOGAI PI , TETSUO NISHIKAWA, PI YURI KAWAI PI YURI KAWAI PC C12N15/12, C12N5/10, C12N1/15, C12N1/19, C12N1/21, C12P21/02, PC C07K14/47, PC C07K16/18, C12Q1/02, C12Q1/68	
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2 (bases 1 to 2405)
1 sogai, T. and Yamamoto, J.
1 sogai, T. and Yamamoto, J.
Direct Submitsion
Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 229-0812, Japan
(E-mail:genomics@shri.co.jp, Tel:181-438-52-3975, Fax:81-438-52-3986)
HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass
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2405 bp mRNA linear PRI 03-SEP-2002 Homo sapiens cDNA PSEC0067 fis, clone NT2RP2001142, weakly similar to VERY-LONG-CHAIN ACYL-COA SYNTHETASE (EC 6.2.1.-).
AK075377
                                                                                                                                                                                                                     Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K., Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T., Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T.
The human CDNA sequencing project
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ADBGGPEGGCSLAWRLASLAQQRAAHTFLHHGSRRFSYSEABRESURRARAFLALGW
DWGPDGGDSGEGSAGEGERAAPGAGDAAGGGAFAGGGGGAARGLGSQAAPLSPGTVA
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TSGTTGLFKAARISHLKILQCGGFYQLCGVVQEDVIYLALPLYHMSGSLLGIVGCMGI
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YDVTTGBPIRDDGGHCRHATSPGELLVAPVGQGSFUGAVGGCRLLKDVFRP
GDVFRWTGDLLVCDQGFTAFFERNGCENVATTEVAEVFERALDFLCBVNVYG
VTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPPYARPFLRLQESLATTETFK
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precursor cells after 2-weeks retinoic acid (RA)
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/mol_type="mRNA"
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1561 CTTCCCCTTCACTTGATTCGCTATGATGTCACCACAGGAGAGCCAATTCGGGACCCCCA 1620	1501 CATCAACTACACAGGACAGCGGGGCGCTGTGGGGCGTGCTTCCTGGCTTTACAAGCATAT 1560	1441 GCGCTTCGGGCCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGTGGCCAC 1500	1381 TAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCCAGATACCTGGGAGCGTTTTGTGCG 1440	1321 CATTGGGGAGCTGTGCCGATACCTTGTCAACCAGCCCCGGAGCAAGGCAGAACGTGGCCA 1380	1261 GTTCTCGGCTGGTCAGTTCTGGGAAGATTGCCAGCAGCACAGGGTGACGGTGTTCCAGTA 1320	01 TTC	1141 GTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCCACTCTACCACATGTCCGG 1200	1081 CCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATGCCAGGGCTTCTATCAGCT 1140	1021 TTCCCCCCAGAGCATAACAGACACGTGCCTGTACATCTTCACCTCTGGCACCACGGGCCT 1080	961 TAGCGATTTGCTGGAGGTGTCCGCTGAAGTGGATGGGCCAGGACACCTCTC 1020	901 CCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGGCCCAGGAACCCACCC	841 CGCGCGCGCGTGGTGCTGGCGCCAGAGTTTCTGGAGTCCCTGGAGCCGGACCTGCCCGC 900	781 TGCCTTTGTGCCCACCGCCCTGCGCCGGGGCCCCTGCTGCACTGCCTCCGCAGCTGCGG 840	721 CCCCGCTGGCCCAGAGTTTCTGTGGCTCTGGTTCGGGCTGGCCAAGGCCGGCC	661 CGCCAGAGGTGGAGGAGCCGCCGCCCTCTGTCACCTGGAGCAACTGTGGCGCTGCTCCT 720	601 GCCGGGAGCCGGAGATGCAGCGGCCGGAAGCGGCGCGGAGGTTTGCCGGAGGGGACGGTGC 660	თ თ	
AUTHORS Baranova, A.V., Krukovskaya, L.L	Homo sapiens Homo sapiens Eukaryota; Metazoa; Mammalia; Eutheria;	ACCESSION AX677203 1 GI:29334629 VERSION AX677203.1 GI:29334629 VERSION AX677203.1 GI:29334629 VERSION AX677203.1 GI:29334629	AX677203	Db 2401 CCTAC 2405	2341	Db 2281 GGAACTCTGTGGGGTCACTA; Oy 2341 CCAGAACTGGGGTCACTA;	2221	2161	2101	2041	1 1981 1 981	1921	1861 T	1801	1741 1741	1681	Qy 1621 GGGGCACTGTATGGCCAC Db 1621 GGGGACTGTATGGCCAC	1561
Yankovsky,N.K., Kozlov,A.P., Lobashev,A.V. and	Chordata; Craniata; Vertebrata; Euteleostomi Primates; Catarrhini; Hominidae; Homo.	ŗ	2430 bp DNA linear PÀT 27-MAR-2003			CGARCIC IN INCOME INCOME IN THE PROPERTY OF	CGCCCTCCTGGCAGGAAACCTTCGAATCTGAGACTTCCACACCTGGAGGCACCTGAGGAA	ACTGTACGTTCTGGACCAGGCTGTAGGTGCCTACCTGCCCCTCACAACTGCCCCGGTACAG 	CAAACAGCAGAAAGTTCGGATGGCAAATGAGGGCTTCGACCCCAGCACCCTGTCTGACCCC 	ACCITATGCCCGGCCCGATTCCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTT	GGGTCCCCCCAGGCTTTGGACCTTATGCAGCTCTACACCACGTGTCTGAGAACTTGCC	GETCTATGGAGTCACTGTGCCAGGGCATGAAGGCAGGCTGGAATGGCAGCCCTAGTTCT	TGTGGCCACAACCGAGGTGGCAGAGGTCTTCGAGGGCCCTAGATTTTCTTCAGGAGGTGAA	CAAGGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAGAGGGGAGAA	GARIGICITECGGCCIGGGARGITITECTICAACACTIGGGGACCTGCTGGTCTGCGATGA	GCAGTCCCCATTCCTGGGCTATGCTGGCGGGCCAGGCTGGCCCAGGGGAAGTTGCTAAA	GGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGTGGCCCCGGTAAGCCA 	CTTCCCCTTCTCCTTGATTCGCTATGATGTCACCACAGGAGAGCCAATTCGGGACCCCCA

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1861 TGTGGCCACAACCGAGGTGCACAAGGTCTTCGAGGCCCTAGAITTTCTTCAGGAGGTGAAAGGTCTTCGAGGCCCTAGAITTTCTTCAGGAGGTGAAAGGTCTTCGAGGCCCTAGAITTTCTTCAGGAGGTGAA	748 0	1628 GGGCACTGTAIGGCCACAICTTCCANGIGNGCCANGGCCACAGGCCACGGGAAGTTGCTAAA 1681 GCAGTCCCCATTCCTGGGGTAIGCTGGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAA	N O O	1448 GCGCTTCGGGCCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGIGGCCA 1501 CATCAACTACACAGGACAGCGGGGCGCTGTGGGGGTGCTTCCTGGCTTTACAAGCATA' 	1301	21 CATTGGGGAGCTGTGCCGATACCTTGTCAACCAGCCCCGAGCAAGGCAGGC	1261 GTTCTCGGCTGGTCAGTTCTGGGAAGATTGCCAGCAGCACAGGGTGACGGTGTTCCAGTA	1201 TTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTGGTGCTGAAAT	1141 GTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCCACTCTACCACATGTCCGG	1081 CCCCAAGGCTGCTCGGATCAGTCTGGAAGATCCTGCAATGCCAGGGCTTCTATCAGCT	21 TTCCCCCAGAGCATAACAGACACGTGCCTGTACATCTTCACCTCTGGCACCI	961 TAGCGATTIGCTGGCTGAAGTGTCCGCTGAAGTGGATGGCCAGTGCCAGGATACCTCTCT	

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                                                                                                                                                                                                              TITLE
        JOURNAL
                                                                                                                                          RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diacchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Boaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2408
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Submitted (06-FEB-2001) National Institutes of Health, Mammalian
                                Strausberg, R. Direct Submission
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Homo sapiens solute carrier family 27 (fatty acid transporter),
member 3, mRNA (cDNA clone MGC:4365 IMAGE:2822875), complete cds.
BC003041
BC003041.1 GI:12804360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2430)
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ORIGIN
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     Query Match

Best Local Similarity

Matches 2405; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Series: IRAL Plate: 9 Row: n Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 132
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               info@bcgsc.bc.ca
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               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="Locusid:11000"
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DWGCDGGGSGSGAGGGRAAPGAFAGDGAAARGGGAAAPLSGGATVA
LLLPAGFEFELWAWGGLAFAFFVFFALRRGPLHCLRSCGARALVAREFLESLE
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TSCTTGLFRAARISHKLIQCQGFYQLCGVHQEDI'INALPYHMSGSLLGI'VGCMGI
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LRPDTWERFVRRFGPLQVLETYGLTGNVATINYTGQRGAVGRASWLYKHIFPFSLIR
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GDVFFNTGDFLVCDQGFLENHDRTGDTFFRKGGNVATITYALPFFBLDFLGEVNVVG
VTVPGHGGRAGWAALVLRPPHALDLNQLYTHVSENLPPYARFRFLKLQESLATTETFK
                                                                                                                                                                                                                                                                                                                                         /note="CaiC; Region: Acyl-CoA synthetases
(AMP-forming)/AMP-acid ligases II [Lipid metabolism./
Secondary metabolites biosynthesis, transport, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQKVRMANEGFDPSTLSDPLYVLDQAVGAYLPLTTARYSALLAGNLRI" 711. .2147
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/protein_id="AAH03041.1"
/db_xref="GI:12804361"
                                                                                                                                                                                                                                                 db_xref="CDD:COG0318"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SLC27A3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="synonyms: FATP3,
/db_xref="LocusID:11000"
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/note="Vector: pOTB7"
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="Lung, small cell
clone_lib="NIH_MGC_7"
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          0
     Score 2405;
Pred. No. 0;
0; Mismatches
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Gaps
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Qy	da VQ	\$ Q	Db Qy	D Qy	D Qy	g V	Qy	45 A	Qy Db	gg Qy	dg VQ	φy	d d	do dy	Qу	Qy Db	Оy	Дb
1081 CCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATGCCAGGGCTTCTATCAGCT 1140	1021 TTCCCCCCAGAGCATAACAGACACGTGCCTGTACATCTTCACCTCTGGCACCACGGGCCT 1080	961 TAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATGGGCCAGTGCCAGGATACCTCTC 1020	901 CCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGGCCCAGGAACCCACCC	841 CGCGCGCGCCCTGGTGCTGGCGCCAGAGTTTCTGGAAGTCCCTGGAAGCCGGACCTGCCCGC 900	781 TGCCTTTGTGCCCACCGCCCTGCGCCCGGGGCCCCCTGCTGCACTGCCTCCGCAGCTGCGG 840	721 CCCCGCTGGCCCAGAGTTTCTGTGGCTCTGGTTCGGGCCAAGGCCAAGGCCGGCC	661 CGCCAGAGGTGGAGGAGCCGCCCCCCCTCTGTCACCTGGAGCAACTGTGGCGCTGCTCCT 720	601 GCCGGGAGATGCAGCGGCCGGAAGCGGCGCGGAGTTTGCCGGAGGGGACGGTGC 660	541 CTGGGGACCCGACGCGACAGCGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGCAGC 600	481 AGAGGCGGAGCGCGAGAGTAACAGGGCTGCACGCGCCTTCCTACGTGCGCTAGGCTGGGA 540	421 GGCCAGCAGCGCGCACACCTTTCTCATTCACGGCTCGCGGGCGCTTTAGCTACTC 480	361 TGCCGCCGACCCGGAAGGTCCCGAGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAACT 420	301 CTTTGCGGTGCGAGCTCTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGCG 360	241 GCTGCTGCTGAAGCTACACCTCTGGCCGCAGTTGCGCTGCCTTCCGGCGACTTGGC 300	181 GATAGAGGAAGCGGCTCCAIGGCTGCCCCTGCTGCCCCCTGCTGCTGCTACC 240	121 CCTAGGTTTTCGGAAGGGAGGATCAGGGATGTTTGCGAGCGGCTGGAACCAGACGGTGCC 180 	61 GGGCGTGTGCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGC 120	
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	108 CANACAGCAGAAAGTTCGGATGGCAAATGAGGGCTTCGACCCCAGCAGCACCCTGTCTGACCC	048 ACCTTATGCCCGGCCC	988 GCGTCCCCCCCACGCTTTGGACCTCTAAGACTCTACACCCACGTGTCTGAGAAACTTGCC				748 6	88 41	628 681	CTTCCCCTTCTCCT GGGGCACTGTATGG						261 GTTCTCGGCTGGTCAGTTCTGGGAAGATTGCCAGCAGCACCAGGGTGACGGTGTCCAGGTA 1		3CTGCTCGGATCAGTCATCTGAAGATCCT 3TCCACCAGGAAGATGTGATCTACCTCGC

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Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyaki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,

Fahey, J., Halton, E., Ketteman, M., Madan, A., Rodrigues, S.

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Schnerch, A., Schein, J. B., Jones, S.J. and Marra, M.A.
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cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurac
Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mc
On Aug 19, 2003 this sequence
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                            Submitted (02-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schnerch,A., Schein,J.E., Jones, S.J. and Flatter,..... Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2430)
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                                                                                                                                                                                                                                                                                                  http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                      version replaced gi:14602825
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Query Match
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Matches 2405; Conserv
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13236578.
                                        CTTTGCGGTGCGAGCTCTGTGCCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGC 360
                                                                                                                                                                    GCTGCTGCTGAAGCTACACCTCTGGCCGCAGTTGCGCTGGCTTCCGGCGGACTTGGC
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PDLPALRAMGLHLMAAGPGTHPAGISDLAEWSAEVDGPVPGYLSSPQSITDTCLYIF

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LRPDTWERFVXREGPLQVLETYGLTEGNVATINYTGQRGAVGRASWLYKHIPPFSLIR

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GDVFRYTGDLLVCDDQGFLRFHDTGOTFRWGGENVATITEVAEVFEALDFLQSVNVG

VTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPPYARPRFLRLQESLATTETFK

QQKVRWANNEGFDPSTLSDPLKVLDQAVGAYLPLTTARYSALLAGNLRI"
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ADPEGPEGGCSLAWRLAELAQQRAAHTFLIHGSRRFSYSEAERESNRAARAFLRALGW
DWGPDGGDSGEGSAGEGERAAPGAGDAAAGSGAEFAGGDGAARGGGAAAPLSPGATVA
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/db_xref="CDD:pfam00501"
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/note="synonyms: FATP3,
/db_xref="LocusID:11000
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/clone lib="NIH MGC 7"
/lab_host="DH10B-R"
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/clone="MGC:2739 IMAGE:2822875"
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mol_type="mRNA"
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1381 TAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCCAGATACCTGGGAGCGTTTTGTGCG 1440	8. TOCCOCCAGGANGTICCOGGANGTICCOCCAGGAGGATTCAGGCCTGGAGGATTAGCTAGT 477 12.1 GGCCCAGCAGCGGCGACAAACCTTTCTCATTCAGGCTGGGGGCTTTAGCTACTC 480 12.1 GGCCCAGCAGCGGCGACAAACCTTTCTCATTCAGGCTGGGGGGCTTTAGCTACTC 480 12.2 GGCCCAGCAGCGGCGAAAATAACAGGCTGCAAGGCCTTGAGGCGGGGGCTTTAGCTACTC 487 12.3 GGCCCAGCAGCGGCGAAAATAACAGGCTGCAAGGGCCTTGAAGAAGGCGAAGCGGGGGCTTAGCTAGC	361 TGCCGCCGAACCCGGAAGGTCCCGAGGGGGGGCCTGCAGCCTTGGCGCGCTCGCGGAACT 420
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Patent: WO 0121795-A 116 29-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH
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GATVVLKSKFSAGGFWEDCQCHRTVTGYIGITGCKAVGRAVGSG
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VTVPGHEGGAGMAALVLRPPHALDIMQLYTHVSENLPFYARFRFLRLQSSLATTETFX
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/db_xref="REMTREMBL:CAC36515"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AY358409.1 GI:37181942
FLI_CDNA.
Homo sapiens (human)

Homo sapiens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 24.14)

Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,

Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,

Dowd, P., Eaton, D., Foster, J., Grimadi, C., Gu, Q., Hass, P.E.,

Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S.,

Hee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,
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Direct Submission
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The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:
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Oy 1758 GGGATGTTTTCTTCAACACTGGGACCTGCTGGTCTGCGATGACGATGTCTCTCCGCT 1817 Db 1814 GGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAAGGTTTTCTCCGCT 1873 Oy 1818 TCCATGATCGTACTGGGACACCTTCAGGTGGAAGGACAAGGTTTTCTCCGCT 1877 Db 1874 TCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAAATGTGGCCACAACCGAGG 1877 1878 TCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGGAAATGTGGCCACAACCGAGG 1933 Oy 1878 TGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATGGAGTCACTG 1937 1934 TGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAAGGTGAACGTCTATGGAGTCACTG 1993	1634 Triciciantianticacia chacadacia anticicia	Db 1514 AGGTGCTGGAGACATATGGACTGACAGAGGGCAACCATCAACTACACAGGAC 1573 Qy 1518 AGCGGGGCGCTGTGGGGCTTCCTGGCTTTACAAGCATATCTTCCCTTTGA 1577 Db 1574 AGCGGGGCGCTGTGGGGTGCTTCCTGGCTTTACAAGCATATCTTCCCCTTTGA 1577 AGCGGGGGCCTGTGGGGGGTGCTTCCTGGCTTTACAAGCATATCTTCCCCTTTCTCCTTTGA 1633 Qy 1578 TTCGCTATGATGTCACCACAGGAGAGCCAATTCGGGGAACCCCCAGGGGCACTGTATGGCCA 1637	1394 GATACCTTGTCAACCAGCCCCCAAGCAAGCCAGAACGTGGCCATAAGGTCCGGCTGGCAG 14 1398 TGGGCAGCGGGCCCAGATACCTGGGAGCGTTTTGTGCGGCGCTTCGGGCCCCTGC 14 1398 TGGGCAGCGGGCCCAGATACCTGGGAGCGTTTTGTGCGGCCCTTCGGGCCCCTGC 14 1454 TGGGCAGCGGGCCCAGATACCTGGGAGGGGACGTTTTGTGCGGCCCTTCGAGCCCCTGC 15		1098 TOAGTCATCTGAAGATCCTGCAATGCCAAGAGGTTCTATCAGCTGTGTGTG	1038 CAGACACGTGCCTGTACATCTTCACCTCTGGCACCACGGGCCTCCCCAAGGCTGCTCGGA 109	Qy 918 TCCACCTGTGGGCTGCAGGCCCAGGAACCCACCCTGCTGGAATTAGCGATTTGCTGGCTG	Qy 858 TGGCGCCAGAGTTTCTGGAGTCCCTGGAGCCGGACCTGCCCCCCTGAGAGCCATGGGGC 917

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                                                                            Isogai, T. and Yamamoto, J.

Direct Submission
Submitted (15-JHL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Submitted (15-JHL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(B-mail:genomics6hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'-& 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AK125102.1 GI:34531083 oligo capping; fis (full insert sequence) Homo sapiens (human)
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3343 bp
Homo sapiens cDNA FLJ43112 fis,
to Homo sapiens VLCS-H1 protein
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                            Location/Qualifiers
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weakly similar
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Query Match Best Local Similarity Matches 2398; Conserv 1246 1186 1366 1306 1126 1066 1426 301 481 421 361 241 121 946 6 μ GCCGGGAGCCGGAGATGCAGCGGCCGGAAGCGGCGGAGTTTGCCGGAGGGGACGGTGC CTGGGGACCCGACGGCGACAGCGAGGGGGAGGAGGGGAGAAAGAAAGGCGAGCAAGCGGGCAAGC GGCCCAGCAGCGCGCCGCCACACCTTTCTCATTCACGGCTCGCGGCGCCTTTAGCTACTC TGCCGCCGACCCGGAAGGTCCCGAGGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAACT TGCCGCCGACCCGGAAGGTCCCGAGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAACT gengengengengaagenacaeenengeeeeekanneegengeenneeeeeeekaennege GCTGCTGCTGCTGAAGCTACACCTCTGGCCGCAGTTGCGCTGGCTTCCGGCGGACTTGGC GATAGAGGAAGCGGGCTCCATGGCTGCCCCTGCTGCTGCTGCTGCTGCTACC GATAGAGGAAGCGGGCTCCATGGCTGCCCCCTCCTGCTGCTGCTGCTGCTGCTGCTACC CCTAGGTTTTCGGAAGGGAGGATCAGGGATGTTTGCGAGCGGCTGGAACCAGACGGTGCC GGGCGTGTGCCAGCGCACGCGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGC AGAGGCGGAGCGCGAGAGTAACAGGGCTGCACGCGCTTCCTACGTGCGCTAGGCTGGGA AGAGGCGGAGCGCGAGAGTAACAGGGCTGCACGCGCTTCCTACGTGCGCTAGGCTGGGA GGCCCAGCAGCGCGCCCCCCACACCTTTCTCATTCACGGCTCGCGGCGCTTTAGCTACTC CTTTGCGGTGCGAGCTCTGTGCTGCAAAAAGGGCTCTTCGAGCTCGCGCCCCTGGCCGCGC CTTTGCGGTGCGAGCTCTGTGCCAAAAAGGGCTCTTCGAGCTCGCCCCCTGGCCGCGGC CCTAGGTTTTCGGAAGGGAGGATCAGGGATGTTTGCGAGCGGCTGGAACCAGACGGTGCC GGGCGTGTGCCAGCGCACGCGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGC Conservative 0, Score 2387; DI; Pred. No. 0; 0; Mismatches °. Indels 1; Gaps 360 1485 1425 1365 1305 1065 540 480 420 120 60 660 1545 600 1245 1185 240 1125 180 1005 300

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AUTHORS TITLE JOURNAL	1501 CATCAACTACACAGGACAGCGGGGGGGGGGTGCTGCGGGCTTTACAAGCATAT 1560
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870 TICTGGAGICCCTGGAGCCGGACCTGCCCGCCTGAGAGCCATGGGGGTCCACCTGTGGG 929	810 GCCCCCTGCTGCACTGCCTCCGCAGCTGCGCGCGCGCGCG	750 GGTTCGGGCTGGCCAAGGCCGGCCTGCGCACTGCCTTTGTGCCCACCGCCCTGCGCCGGG 809	690 TGTCACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCCAGAGTTTCTGTGGCTCT 749	o gcggcgcgaagttigccggaaggaaggatgcacgccaagaggtggaagaagccc	570 AGGGGAGCGCTGGAGAAGGCGAGCGGGAAGCCGGAAGATGCAGCGGCCGGAA 629	510 CACGCGCCTTCCTACGTGCGTAGGCTGGGACTGGGGACCCGACGGCGACAGCGGCG 569	450 TCATTCACGCCTCGCGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAACAGGGCTG 509	390 GCTGCAGCCTGGCCTGGCGCAGAACTGGCCCAGCAGCGCGCGC	330 GGGCTCTTCGAGCTCGCGCCCTGGCCGGGCTGCCGCCGAACGCTGCCGAGGGGG 389	270 CGCAGTTGCGCTGGCTTCCGGCGGACTTGGCCTTTGCGGTGCGAGCTCTGTGCTGCAAAA 329	210 TCCTGCTGCTGCCCCTGCTGCTGCTACCGCTGCTGCTGCTGCTACACCTACTGGC 269	150 TGTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGCGGGCTCCATGGCTGCCC 209	90 GGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTTCGGAAGGGAGGATCAGGGA 149 	Ouery Match 96.1%; Score 2310.8; DB 6; Length 2314; Best Local Similarity 99.9%; Pred. No. 0; Matches 2312; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	HVSENIAPPELATION TETTETEKQQXVRMANEGFDPSTLSDPLYVLDQAVGAY LPLTTARYSALLAGNLRI"	HORDY PURFYER LIBSEGGEL IN CHIEF EGGE VERFANT SHIDT INCOGE TO THE COMMENT OF THE	HGSRRFSYSEAERESNRAARAFLRALGWDWGPDGGDSGEGSAGEGERAAPGAGDAAAG SGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGLAKAGLRTAFVPTAL RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGGTIPPAGISDLLA	
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Query Match 96.1%; Score 2310.8; DB 6; Length 2314; Best Local Similarity 99.9%; Pred. No. 0; Matches 2312; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Matches 2312; Conservative 0; Mismatches 2; Indels 0; Gaps 0; 90 GGAAGGAGAGTCTCAGCTAGAACGAGCCCTAGGTTTTCGGAAGGGATCAGGA 149	C12N15/09,CO7K14/47,CO7K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/PC 10, PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers FT CDS (60). (2159). FEATURES Location/Qualifiers SOURCE /organism="Homo sapiens" /mol_type="genomic DNA" /mbl_type="featon:9606" ORIGIN	TITLE Primer for synthesizing full-length cDNA and use thereof JUURNAL Patent: JP 2002191363-A 14456 09-JUL-2002; HELIX RESEARCH INSTITUTE COMMENT OS Homo sapiens (human) PN JP 2002191363-A/14456 PD 09-JUL-2002 PF 28-JUL-2000 JP 2000280990 PF 28-JUL-2000 JP 2000280990 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU PI SAITO, PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAWA, AI WAKAWATSU, PI KEIICHI NAGAI, TETSUJI OTSUKI PC KEIICHI NAGAI, TETSUJI OTSUKI	KEYWORDS JP 2002191363-A/.4456. KEYWORDS JP 2002191363-A/.4456. SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 2314) AUTHORS Ota.T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.	SULT 11 159613 CUS BD159613 FINITION Primer for synthesizing full-length c CESSION BD159613 8570N BD159613	2310 GTGTACTGGGCTGTCAGGGATCTTTTCTATACCAGAACTGCGGTCACTATTTTGTAATAA	2041 AGGGTTCGACCCCAGCACCCTGTCTGACCCACTGTACGTTCTGGACCAGGCTGTAGGTG 2190 CCTACCTGCCCCTCACAACTGCCCGGTACAGCGCCCTCCTGGCAGGAAACCTTCGAATCT	Db 1921 AGCTCTACACCCACGTGTCTGAGAACTTGCCACGTAAGGACCTGTACGGATTCCTCAGGC 1980 Qy 2070 TCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAGTTCGGATGGCAAATG 2129 Db 1981 TCCAGGAGTCTTTGGCCACCAGAGAGACCTTCAAACAGCAGAAAGTTCGGATGGCAAATG 2040 2130 AGGGCTTCGACCCCAGGACCCTGTCTGACCCACTGTACGTTCTGGACCCAGGCTTTAGGTG 2189
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AGATCCTGCAATGCCAGGCTTCTATCAGCTGTGTGTTCTCCAGGAAGATGTGATCT 118	GCTGGCTGAAGTGTCCGCTG 989	CCGCCCTGCGCCAGAGT 8		CACGCGCCTTCCTACGTGCGCTACGCTAGGCTGGGACTGGGGACCCGACGCGCGCG	GCTGCAGCCTGGCGCTCGCGGAACTGGCCCAGCAGCGCGCGC	TCCTGCTGCTGCCCCTGCTGCTGCTACCGCTGCTGCTGCTGAAGCTACACCTCTGGC 180 CGCAGTTGCGCTGGCTTCCGGCCGACTTGGCCTTTGCGGTGCGACTCTGTGCTGCAAA 329 [GGGAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTTCGGAAGGGAGGATCAGGGA 60 TGTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGCGGGCTCCATGGCTGCCC 209 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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00	CCACTGTACGTTCTGGACCAGGCTGTZ 	B 8
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6 49	1890 TCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTAIGGAGTCACTGTGCCAGGGCATG 19	용 성
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8 6	1710 GGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGGATGTCTTCCGGCCTGGGGATGTTTTCT 17	B 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
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Homo sapiens cDNA FLJ14593 fis, clone NT2RM4002073, m
similar to Mus musculus fatty acid transport protein
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Isogai,T. and Otsuki,T.
Direct Submission
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RYSAEVDGPVPGYLSSFQSITDTCLYIFTSGTTGLFKAARISHKILQCQGFYQLCGV
HQEDVIYLALFLYHMGGSLLGIVGYOMGATVYLXSKESAGQFWEDQOULRTVTVGYJ
GELCRYLVNQPPSKAERGHKVRLAVGSGLRPDTWERFVRRFGFLQVLETYGLTEGNVA
TINYTGGRGAVGRASWLYKHIFFFSLIRYDVTTGEFRAFGFDQHCMATSFGEFGLLVAF
VSQQSPFLGYAGGPBLAQGKLLKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFR
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HVSENLPPYABPRFILRLQESLATTETFKQQKVRMANEGFDPSTLSDFLYVLDQAVGAY
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1050 TGTACATCTTCACCTCTGGCACCACGGGCCTCCCCAAGGCTGGTCGGATCAGTCAG	990 AAGTGGATGGGCCAGTGCCAGGATACCTCTCTCTCCCCCCAGAGCATAACAGACACGTGCC 1049	930 CIGCAGGCCCAGGAACCCACCCTGCTGGAATTAGCGATTTGCTGGCTG	870 TICTGGAGTCCCTGGAGCCGGACCTGGCCCCTGAGAGCCATGGGGCTCCACCTGTGGG 929	810 GCCCCTGCTGCACTGCCTCCGCAGCTGCGGCGCGCGCGCG	750 GGTTCGGGCTGGCCAAGGCCGGCCTGCGCACTGCCTTTGTGCCCACCGCCCTGCGCCGGG 809	690 TGTCACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCCAGAGTTTCTGTGGCTCT 749	630 GCGGCGCGAGATTTGCCGGAGGGGACCGTGCCGCCAGAGGTGGAGGAGCCGCCCCCCC 689	570 AGGGGAGCGCTGGAGAAGGCGAGCGGCAGCGCCGGGAGACCCGGAGATGCAGCGGCCGGAA 629	510 CACGCGCCTTCCTACGTGCGCTAGGCTGGGACTGGGGACCGACGGCGGCGACAGCGGCG 569	450 TCATTCACGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGAGCGCGAGAGTAACAGGGCTG 509	390 GCTGCAGCCTGGCCGCCGCGGAACTGGCCCAGCAGCGCGCGC	330 GGGCTCTTCGAGCTCGCGCCCTGGCCGGCGGCTGCCGGCGGAAGGTCCCGGAGGGGG 389	270 CGCAGTIGCGCTGCCTTCCGGCGACTTGCCGGTGCGAGCTCTGTGCTGCAAAA 329	210 TCCTGCTGCCCCTGCTGCTGCTACCGCTGCTGCTGCTGAAGCTACACCTCTGGC 269	150 TGTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGCGGGCTCCATGGCTGCCC 209	90 GGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTTCGGAAGGGAGGATCAGGGA 149 	Match 96.1%; Score 2310.8; DB 9; Length 2314; cal Similarity 99.9%; Pred. No. 0; Similarity 99.9%; Pred. No. 0; Gaps 0; S 2312; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
D 49	9. g	Q B K	Q & .	Q B .	ο β <i>κ</i>	}	g 8	Q	O B 4	Q B !	S B 8	S B 7	S B :	o Br	S B 7	O B 1	S B 1	0
AGGCTTCGACCCCAGCACCCTGTCTGACCCACTGTACGTTCTGGACCAGGCTGTAGGTG 210					TIGARGACACTICATULA CANAGOGAGAATGTGGCCAACGAACGTGAACGAAGGAAGGTCAACGAAGGAAG	1 CAACACAGGGACCAGCAGAAAAAAAAAAAAAAAAAAAA	621 GGCAGAGCTGGCCCAGGGGAAGTTGCTAAAGGATGTCTTCCGGCCTGGGGATGTTTTCT 168		TO AGCCAGGAGTGGTGGTGGCCCGGTAAGCCAGTAGTCCCCATTCCTGGGGTATGCTGGGGG 170									1110 AGATCCTGCAATGCCAGGGCTTCTATCAGCTGTGTGTGTCCACCAGGAAGATGTGATCT 1169

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Wadan, A., Kodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
DNA sequences
DNA sequences
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                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Baylor College of Medicine Human Genom
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission

Direct Submission

Marional Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                      Sequencing Center
Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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FEATURES Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gseries: IRAK Plate: 50 Row: n Column: 23. A.N., Gibbs, R.A. Location/Qualifiers

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GELCRYLVNQPPSKAERGHKVRLAVGSGTRAFTTTGEPVBAGGTWATSPGEPGLLVAP
VSQOSPFLGYAGRASWLYKHIFPFSLLRYDVTTGGPIRDPGGHCMATSPGEPGLLVAP
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WKGENVATTEVAEVFEALDFIQEVNVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYT
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/note="CaiC; Region: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Lipid metabolism Secondary metabolites biosynthesis, transport, and _xref="CDD:COG0318"

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Length 2333;

Matches 2280; Query Match Best Local Similarity 366 181 306 121 246 186 126 GTTTTCGGAAGGGATCAGGGATGTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAG 185 5 \vdash AGCAGCGCGCGCGCACACCTTTCTCATTCACGGCTCGCGGCGCTTTAGCTACTCAGAGG CCGACCTGGAAGGTCCCGAGGGGGGGCTGCAGCCTGGCGGCCTCGCGGAACTGGCCC CGGTGCGAGCTCTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCG TGCTGCTGAAGCTACACCTCTGGCCGCAGTTGCGCTGGCTTCCGGCGGACTTGGCCTTTG TGCTGCTGAAGCTACACCTCTGGCCGCAGTTGCGCTGGCTTCCGGCGGACTTGGCCTTTG AGGAAGCGGGCTCCATGGCTGCTGCTGCTGCTGCTGCTGCTGCTACCGCTGC GTTTTCGGAAGGGATCAGGGATGTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAG CCGACCCGGAAGGTCCCGAGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAACTGGCCC Conservative 94.8%; CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCCGGCTGCCG 0 Score 2280; Pred. No. 0; Mismatches 0 Indels 0 Gaps 305 425 240 365 120 245 60 485 300 180

26 GGGAGCTGTGCCGATACCTTGTCAACCAGCCCCGAGCAAGGCAGAACGTGGCCATAAGG 1385	01 AGCAGGGGGGGGGAACACCTITCTCATTCACGGCTGGGGGCTTTAGCTACTCAGAGG 86 CGGAGGGGGAAGAACACCTTCTACTCATAGCTACTCAGAGG 87
RESULT 14 AR168916 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES	\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$
14 16 AR168916 AR168916 TION Sequence 101 from patent US 6288213. AR168916 N AR168916 Unknown. Unknown. Unclassified. Unclassified. Unclassified. 1 (bases 1 to 2166) CRS Stahl, A., Hirsch, D.J., Lodish, H.F., Gimeno, R.E. and Tartaglia, L.A. E Fatty acid transport proteins Fatty acid transport proteins NAL Patent: US 6288213-A 101 11-SEP-2001; ES Location/Qualifiers	1566 CCTTCTCCTTGATTCGCTATGATGCCACCACAGGAGCCCAATTCGGGACCCCCAGGGGGC 1625 1441 CCTTCTCCTGATTCGCTATGGTATGTGCACCACAGGAGCCCAATTCGGGACCCCCAGGGGCC 1625 1501 ACTGTATGGCCACATCTCCAGGTGAGCCACGGGGTGCTGGGGCCCCAGGGGCAACTCGCCCAGGGCCAATTCGGGAACCCCCCAGGGCCAATTCGGGACCACGGCCTAGGCCAACGCCCCAGGGCCAACTCCCCAGGGCCAACGCCCCAGGGCCAAGGCCACGGCCTAGGCCAACGCCCCAGGGCCAAGGCCAACGCCCCAGGGCCAAGGCCAACGCCCCAGGGCCAAGGCCAACGCCCCAGGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCAAGGCCAAGGAAACTTCCAAGCCAAGAACCTTCAAAACCTAAGGCAAGGCCAAGAACCTTCAAAACCTAAGGCAAGAACTCAAGAAACCTTCAAAACCTAAGAAACCTTCAAAACCTAAGAAACCTTCAAAACCTAAGAAACCTTCAAAACCTAAGAAACCTTCAAAACCTAAGAAACCTTCAAAACCTAAGAAACCTTCAAAACCTAAGAAACCTTCAAAACCTAAGAAACCTTCAAAACCTAAGAAACCTTCAAAACCTAAGAAACCTTCAAAACCTAAAACCTAAAACCTAAAACCTAAAACCTAAAACCTAAAACATCAAAACCTAAAACCTAAAACATCAAAACCTAAAACCTAAAACATCAAAAACCTAAAACCTAAAACCTAAAACATCAAAACCTAAAAACCTAAAAAA

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Db 1934 GATTCCTCAGGCTCCAGGAGTCTTTCGACCACAGAGAGACCTTCAAACAGCAGAAAGTTC 1993 Oy 2118 GGATGGCAAATGAGGGCTTTCGACCCCAGCACCACCACCACCACCACCACCACCACCACC	OY 1998 TGGACCTTATGCAGCTCTACACCCACGTGTCTGCAGAACTTGCCCACCTTATGCCCGGCCCC 2057	Qy 1878 TGCCAGAGGTCTTCGAGCCCTAGATTTTCTTCAGGCAGGTCAACGTCTACGAGGTCAACGTCTACTG 1937 Db 1754 TGCCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATGGAGTCACTG 1813 Qy 1938 TGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGGCCTAGGTTCTGCGTCCCCCCCACGCTT 1997	1634 GGGATGTTTCTTCAACACTGGGGAACCTGCTGGTCTGCGAAACGTTTTCTCCGCT 1818 TCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGGAGAATGTTGGCCACAACCGAGG 1818 TCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTTGGCCACAACCGAGG 1694 TCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGCCACAACCGAGG 1694 TCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGCCACAACCGAGG	1514 1698 1574	Qy 1578 TTCGCTATGATGTCACCACAGAGAGACCCAATTCGGGACCCCCAGGGGCACTGTATGGCCA 1637	Oy 1458 AGGTGCTGGAGACATATGGACTGACAGAGGCACCGTGCCACTCACCACGAC 1517 Db 1334 AGGTGCTGGAGACATATGGACTGACAGAGGCAACCATCAACTACACAGAC 1393 Oy 1518 AGGGGGGCTGTGGGGGGGTTCCTGGCTTTACAAGCATATCTTCCCCTTGA 1577	1214 GATACCTTGTCAACCAGCCCCCGAGCAAGGCAGAACGTGGCCATAAGGTCCGGCTGGCAG 1398 TGGGCAGCGGGCTGCGCCCAGATACCTGGGAGCGTTTTGTGCGGCGCTTTCGGGCCCCTGC	1278 1154 1338	OY 1158 AGATGTGATCTACCTCGCCCTCCCACTCTACCACATGTCCGTCTGCTGGGCATCG 1217	TGTCC/

Qy 501 ACAGGCTGCACGCGCTTCCTACGTGCGTAGGCTGGGAACTGGGAACCGGACGCGCGCG	321 GUINAMANGGUILLI CHAGUI CUCUCUCUCUCUCUCUCUCUCUCUCUCUCUCUCUCUC	14 CGGGATGTTTGCGAGCGGCTGGAACCAGACGATGCCGATAGAGCAAGCGGCTCCATGG 204 CTGCCCTCCTGCTGCTGCTGCTGCTGCTGCTACCGCTGCTGCTGAAGCTAC	/mol_type="unassigned DNA" IGIN 88.1%; Score 2119.4; DB 6; Length 2166; Best Local Similarity 99.7%; Pred. No. 0; Matches 2146; Conservative 0; Mismatches 1; Indels 6; Gaps Matches 2146 CAGGGATGTTTGCGAGCGGCTGCATGG 144 CAGGGATGTTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGCGGGCTCCATGG	Unknown. Unknown. Unclassified. 1 (bases 1 to 2166) 1 (bases 1 itsch,D.J., Lodish,F. Stahl,A., Hirsch,D.J., Lodish,F. Methods of identifying agents i proteins Patent: US 6348321-A 101 19-FEE Location/Qualifiers 1 2166 /organism="unknown".	RESULT 15 AR193703 AR193703 LOCUS AR193703 2166 bp DNA linear PAT 20-APR-2002 DEFINITION Sequence 101 from patent US 6348321. ACCESSION AR193703 VERSION AR193703.1 GI:20240295 KEYWORDS .	Db 2054 AGGCTGTAGGTGCCTACCTGCCCCTCACAACTGCCCGGTACAGCGCCCTCCTGGCAGAA 2113 Qy 2238 ACCTTCGAATCTGAGAACTTCCACACCTGAGGCACGTAGAGAGAACTCTGT 2290
Db 1454 TTCGCTATGATGTCACCAGAGAGAGCCAAATTCGGGAACCCCAAGGGGCCCCT 1813 Oy 1638 CATCTCCAGGTGAGCCAAGGGGTGCTGGTGGCCCCGTTATGGCCA 1597 Db 1514 CATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCAGCAGTCCCCATTCCTGG 1697 OY 1698 GCTATGCTGGCGGGGCCAGAGCTGGCCCAGGGGAAGTTCCTAAAGGATGTCTTCCTGGCCTG 1757 OD 1574 GCTATGCTGGCGGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGGATGTCTTCCGGCCTG 1693 OY 1758 GGGATGTTTCTTCAACACTGGGGACCTGGTGGTCGCAAAGGATGTCTTCCCGCCT 1817 Db 1634 GGGATGTTTTCTTCAACACTGGGGACCTGCTGGTTGCTGCAAAGGATGTTTCTCCCCCT 1817 OY 1818 TCCATGATCGTACTGGAAGACCCTTCAGGTGGAAAGGAATGTTGGCCACAACCGAAG 1877	Db 1274 TGGGCAGCGGGCTGCGCCCAGATACCTGGAACGTTTTTGTGCGGCCCTTTCGGCCCCTGC 1333 Qy 1458 AGGTGCTGGAACATATGGACTGACAGAGGGCAACGTGGCCACCATCAACTACACAGAGAC 1517 Db 1334 AGGTGCTGGAGACATATGGACTGACAGAGGGCAACGTGGCCACCATCAACTACACAGAGAC 1393 Qy 1518 AGCGGGGCGCTGTGGGGTGCTTCCTGGCTTTACAAGCATATCTTCCCCTTGA 1577 Db 1394 AGCGGGGCGCTGTGGGGGTGCTTCCTGGCTTTACAAGCATATCTTCCCCTTGA 1453 Qy 1578 TTCGCTATGATGTCACCACAGGAGAGACCACAGGGCACTGTATGGCCA 1637	OY 1278 TCTGGGAAGATTGCCAGCACAGGGTGACGGTGTTCCAGTACATTGGGGAGCTGTGCC 1377	Db 974 TCAGTCATCAGAGATCCTGCAAGGCTTCTATCAGCTGTGTGTG	978 AAGTGTCCGCTGAAGTGGGATGGGCCAGGAGATACCTCTCTTCCCCCCAGAGCATAA 1	QY 858 TGGGGCCAGAGTTTCTGGAGTCCCTGGAGGCCCTGAGAGGCCATGGGGC 917	Qy 738 TTCTGTGGCTCTGGTTCGGGCTGGCCAAGGCCGGCCTGCGCACTGCTTTGTGCCCACCG 797

	ACCTTCGAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGA	2114	В
	ACCTTCGAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGA	2238	Ş
2113	AGGCTGTAGGTGCCTGCCCCTCACAACTGCCCGGTACAGCGCCCTCCTGGCAGGAA	2054	Βb
2237	AGGCTGTAGGTGCCTACCTGCCCCTCACAACTGCCCGGTACAGGCCCCCCCTGGCAGGAA	2178	Ş
2053	GGATGGCAAATGAGGGCTTCGACCCCAGCACCCTGTCTGACCCACTGTACGTTCTGGACC	1994	Db
2177	GGATGGCAAATGAGGGCTTCGACCCCAGCACCCTGTCTGACCCACTGTACGTTCTGGACC	2118	Ş
1993	GATTCCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAGTTC	1934	g
2117	GATTCCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAGAAAGTTC	2058	γQ
1933	TGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCCCACCTTATGCCCGGCCCC	1874	В
2057	TGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCCACCTTATGCCCGGCCCC	1998	γŞ
1873	TGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCCCCACGCTT	1814	뫄
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1813	TGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATGGAGTCACTG	1754	рb
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JOURNAL MEDLINE PUBMED	TITLE	REFERENCE AUTHORS	PUBMED	MEDLINE	JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AK076014	d a builting of
Drepare rull-rengen come increase to represent the server of the general Genome Res. 10 (10), 1617-1630 (2000) 20499374 11042159	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs of the contraction of cap-trapper selected cDNAs of the cap-tra	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,	10349636	99279253	Meth. Enzymol. 303, 19-44 (1999)	High-efficiency full-length cDNA cloning	Carninci, P. and Hayashizaki, Y.	1	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mus musculus	Mus musculus (house mouse)	HTC; CAP trapper.	AK076014.1 GI:26344941	AK076014	(fatty acid transporter), member 3, full insert sequence.	Mus musculus 10 days embryo whole body cDNA, RIKEN full-length	AK076014 1990 bp mRNA linear HTC 20-SEP-2003		

Result No.

Score

Query Match Length DB ID

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
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                                                                                    /note="unnamed protein product; putative
solute carrier family 27 (fatty acid transporter),
3 (MGD|MGI:1347358, GB|AF072758, evidence: BLASTN,
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                                                                                                                                                            /dev_stage="10 days embryo" 533 ... 1873
/codon_start=1
/protein_id="BAC36120.1"
/db_xref="GI:26344942"
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/clone_lib="RIKEN full-length
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/translation="MGLHLWATGPETNVAGISNLLSEAADQVDEBPVPGYLSAPQNIMD
TCLYIFTSGTTGLPKAARISHLKVLQCQGFYHLCGVHQEDVIYLALPLYHMSGSLLGI
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LAVGSGLRPDTWERFLRRFGPLQILETYGMTEGNVATFNYTGRGAVGRASWLYKHIF
PFSLIRKTDWMTGEFILNAQGHGMTTSPGEPGLLVAPVSQOSPFLGYAGAPBLAKKNLF
KDVFWSGDVFFNTGDLLVCDEQGFLHFHDRTGDTFRWKGENVATTEVAEVLETLDFLQ
EVNIYGYTVPGHEGRAGMALALRFPQALMIVQLYSHVSENLFYARPRIRCLQESLA
TTETFKQKXNEMANEGFDFSVLSDFLYVLDQDIGAYLPLTPARYSALLSGDLRI"
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GATCCTGCAATGCCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTA 1170
                                                                    GTACATCTTCACCTCTGGCACCACGGGCCTCCCCAAGGCTGCTCGGATCAGTCAFCTGAA
                                                                                                                                                         AGTGGATGGCCAGTGCCAGGATACCTCTCTTCCCCCCAGAGCATAACAGACACGTGCCT
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ORGANISM
                                                                                       Nature 420, 563-573 (2002)

12 6 (bases 1 to 2018)

13 Adachi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiramoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Hiramoto, K., Konno, H., Kouda, M., Kotoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Myazaki, A., Murata, M., Nishi, K., Nomura, X., Numaraki, R., Ohno, M., Ohsato, N., Nakamura, M., Nishi, K., Nomura, X., Numaraki, R., Ohno, M., Ohsato, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Taya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
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FANTOM Consortium.
Functional annotation of a
Functional 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Physical and Chemical Research (RIKEN), Laboratory Exploration Research Group, RIKEN Genomic Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                  Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length CDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Pax:81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
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/strain="C57BL/6J"
/db_xref="FANTOM_DB:9930102C17"
/db_xref="MGI:24G1515"
/db_xref="taxon:10090"
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                                                                            AGGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGT
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Query Match 39.2%; Score 942.2; DB 13; Length 997; Best Local Similarity 98.4%; Pred. No. 3.3e-150; Matches 977; Conservative 6; Mismatches 6; Indels 4; Gaps 3;	cedex - France code - France c	RESULT 3 BX354148/C LOCUS BX354148 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens CDNA Clone CSODCO15YH21 3-PRIME, mRNA sequence. BX354148 Homo sapiens CDNA Clone CSODCO15YH21 3-PRIME, mRNA sequence. BX354148 I GI:30373826 VERSION BX354148.1 GI:30373826 SOURCE ORGANISM Homo sapiens CORGANISM Homo sapiens EURATYOLA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 997) AUTHORS Li, M.B., Gruber, C., Jessee, J. and Polayes, D. TITLE Ull-length cDNA libraries and normalization Unpublished (2001) COMMENT Genoscope Genoscope - Centre National de Sequencage	Db 1514 GGCCACACTGAAGTGGCTGAAGTCTTGGAAGCCTTGAGAAGTTGAACAT 1573 Oy 1924 CTATGGAGTCACTGTGCCAGGGCATGAAGGCAGGGTGAAATGGCAAGGCTAGATTCTGCG 1983 1574 CTATGGAGTCACGTTGCCAGGGCATGAAGGCAGGCTGGAATGGCAAGCCTTAGGCTTGCCAGC 1983 1574 CTATGGAGTCACGGTTGGAACCTTATGCAAGCAAGGCATGGCGAGAACTTGCCACC 2043 Oy 1984 TCCCCCCCACGCTTTGGAACCTTATGCAAGCTCTACACCCACGTGTCTGAAACTTGCCACC 2043 Oy 1984 TCCCCCCCACGCTTTGAACCTTGGAAGCTCTACACCCACGTGTTTCTGAAACTTGCCACC 2043 Oy 2044 TTATGCCCGGCCCCGATTCCTCAGGCTCCAAGAGTCTTTGGCCACCAAGAACTTGCCACC 1693 Oy 2044 TTATGCCCGGCCCCGATTCCTCAGGCTCCAAGAGTCTTTGGCCACCAAGAGAACTTCAA 2103 Db 1694 GTATGCCCGACCTCGGTTTCTCAGGCTCCAAGAGATCTTTGGCCACCAAGAGACCTTCAA 1753 Oy 2104 ACAGCAGAAAGTTCGGATGGCAAATGAGGGCTTCGAACCACAAGAGACCTTCAA 1753 Oy 2104 ACAGCAGAAAGTTCGGATGGCAAATGAGGGCTTTGACCCCAACAGAGACCTTCAACCTTCAACCCTTCAACCCTTCAACCCTTCAACCCTTCAACCTTCGAAACCTTCGAAACCTTTGACCCCCAACAACTGCCCCGGTACAGCACCTTCAACCCTTCAACCCTTCGAACCCTTCGAACCCTTCGAACCCTTCGAACCCTTCGAACCCACCTTCAACCCCCTTCAACCCCCTTCAACACCCACCTTCAACACCAC
RESULT 4 EX460000 BX460000 BX460000 1201 bp mRNA linear EST 22-MAY-2003 DEFINITION BX460000 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone	2102 AAACAGCAGAAAGTTCGGATGGCAAATGAGGCTCTGACCCCCAGCACCTGTCTGACCCA 2 2102 AAACAGCAGAAAGTTCGGATGGCAAATGAGGCTCTGACCCCAGCACCACCACAGAGACCTTC 2 2102 AAACAGCAGAAAGTTCGGATGGCAAATGAGGGCTTCGACCCCAGCACCCCTGTCTGACCCA 2 2104	GAACC GAAT GGAAC GAAC GGAAC	Qy 1383 AGGTTCCGGCTGGCAGTGGGCCAGATACCTGGGAGAGCGTTTTGTGCGGC 1442 Db 990 AAGTTCCGGCTGGCAGTGGGC CAGGCGGCCCAGATACCTGGGAGACCTTTTTGTGCGGC 1502 991 A43 GCTTCCGGCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGTGGCCACCA 1502 Db 932 GCTTCCGGCCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGTGGCCACCA 673 Qy 1503 TCAACTACAACAGAACAGGAGGGCGCTTGGAGAGAGGGCAACGTTGACAAGCATATCT 1562 Db 872 TCAACTACAACAGGACAGCGGGGGCGTTGGGGGCTTCCTGGCTTTACAAGCATATCT 813 Qy 1563 TCCCCTTCTCCTTGATTCGCTATGATGTCACCACAGGAGAGCCAATTCGGGAACCCCCAGG 1622 Db 1623 GGCACTGTATGGCCAATCTCCAGGTGAGCCAGGAGAGCCCCCAGG 753 Qy 1623 GGCACTGTATGGCCACATCTCCAGGTGAGCCAGGAGAGCCCCCAGGTAAGCCATTCGGGAACCCCCAGG 1682 Db 1624 GGCACTGTATGGCCACATCTCCAGGTGAGCCAGGAGGCCCCCGGTAAGCCAGC 1682 Qy 1683 AGTCCCCATTCCTGGGCTATGCTGGCCAGAGCTGGGCCCCAGGGAAGTTCGCTAAAGG 1742 Db 692 AGTCCCCATTCCTGGGCTATGCTGGCCAGAGCTGGGCCCCAGGGAAGTTGCTAAAGG 1742 Qy 1743 ATGTCTTCCGGGCTATGCTGGCGAGCCAGAGAGCCCCAGGGAAGTTGCTAAAGG 1742 Qy 1743 ATGTCTTCCGGGCTATGCTTGGCCAGACCAGGAGCCCCAGGGAAGTTGCTAAAGG 1742 Qy 1743 ATGTCTTCCGGGCTATGCTTGGCGAACACACAGGAGAGCCCCAGGGAAGTTGCTAAAGG 634

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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 661.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODF009CC03QF1&cluster=661.f. Contact
Feng Liang Email: fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODF009CC03QF1.
Location/Qualifiers
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1 (bases 1 to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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                                                                                    CTTCGAGCTCGCGCCTGGCCGCGGCTGCCGCCGACCCGGAAGGTCCCGAGGGGGGGCTGC
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/dev stage="fetal"
/dev stage="fetal"
/clone lib="Homo sapiens FETAL BRAIN"
/clone lib="Homo sapiens FETAL BRAIN"
/note="Torgan: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo (dT) primer. Five prime end
enriched, double-strand cDNA was diessted with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
vector. Library was not normalized."
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/db_xref="taxon:9606"
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B; Mismatches 26;
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segret@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 661.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.gi?seq-CSOD1042AF05QP1&cluster=661.f. Contact:
Feng Liang Email: filiang@lifetech.com URL:
http://fullength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODI042AF05QP1.

Location/Qualifiers
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Li W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
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          /mol_type="mRNA"
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                                                               organism="Homo sapiens"
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Primates; Catarrhini; Hominidae;
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Euteleostomi;

EST 05-MAY-2003

1001 993 941 874

821

934 881 814

761 754 701 694 634 581 574 521

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ORIGIN
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/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Pred. No. 5.3e-146;
""matches 9;
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AUTHORS
TITLE
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SOURCE
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1 (bases 1 to 930)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 13, 2001 this sequence version replaced gi:12784822.

Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DB001BC09NP1&cluster=661.f. Cc
egi-bin/cluster.cgi?seq=CS0DB001BC09NP1&cluster=661.f. Cc
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation
Faraday Avenue Genoscope sequence ID : CS0DB001BC09NP1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL521329
930 bp mRNA linear EST 22-MAY-2003
AL521329 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
CDNA Clone CS0DB001YE18 3-PRIME, mRNA sequence.
AL521329
AL521329
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AL521329
AL521329.2 GI:31039632
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BP 191 91006 EVRY cedex - France
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   GGCCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAAGGTTTTTC
                                                                                                                                                                                                                      TGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCAGCAGTCCCCAT
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                                                                                                                 TCCTGGGCTATGCTGGCGGGCAGAGCTGGCCCAGGGGAAGTTGCTAAAGGATGTCTTCC
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/mol_type="mark",
/db xref="taxon:9606"
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/tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
/clone_Tib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
/clone_Tib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
/clone_Tist strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Pred. No. 9.9e-137;
6; Mismatches 8;
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BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 661.f For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSDDC015CD11QP1&cluster=661.f. Contact Feng Liang Email : filang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODC015CD11QP1. FEATURES Location/Qualifiers	NISM Homo Eukar Mamma NCE 1 (b ORS Li,W. E Full- E Full- ORAL Unpub NAL Unpub Conta	RESULT 7 BX354149 LOCUS BX354149 DEFINITION BX354149 Homo sapiens NEUROBLASTOMA COT 25 NORMALIZED Homo sapiens CDNA clone CSODCO15YH21 5-PRIME, mRNA sequence. ACCESSION BX354149 VERSION BX354149.1 GI:30375843 KEYWORDS SOURCE Homo sapiens (human)	Qy 2352 GTCACTATTTTGTAATAAATGTGGCTGGAG 2381 : : : :	151 CAGGAAACCCTCGAATCTGARAACTTCCACACCTGAGGCACCTRAGAGAGGAACTCTGTG 2292 GGGTGGGGGCCGTTGCAGGTGTACTGGGCTGTCAGAGGAACTCTGTG			1932 TCACTTTATAGAAGTCTTATAAGGCAGGTGAAGAAAGTTTATGCAGCCCCCCCC	
pb 710 ccccrrgraccrgaacaacrgragacaacrgccrccrcccccaaaagrracrgr 769 744 ggcrcrggraccrgaaggcaaaggcagccrgcacacrgccrracacaaagrraccrgc 803	Cy 54 CCGCCACGGAGGGAGCCTGGAACAGCGAGGAGCCCCAGAGTTGCAGCCG 64 CCGGAAGCGGCGGAGGTTTGCCGGAGGGAGCGCCAGAGGTGGAGGAGCCGCG 65 CCGGAAGCGGCGGAGGTTTGCCGGAGGGACGGTGCAGAGGTGGAGGAGCCGCG 66 CCGGAAGCGGCGGAGGTAGCCGAGGGACGGTGCCGCCAGAGGTGGAGGAGCCGCCG 67 68 CCCGGAAGCGGCGGAGCTACCTGGAGGAGCTGCCCCGCCTGGAGGTGGAGGAGCCCCGCCGCCGCCGAGAGTTTTCTGT 68 CCCGGAAGCGGCCGGAGCGAGCGAGCGACGGTGCCCCCCCC	. 444 . 472 . 504 . 531	Db 352 GCAAAARGGCTCTTCGAGCTCGGCCGGCCGCCGCCGGCGGCGCGCGC	ОУ 264 Db 292 QУ 324	Qy 144 Db 172 Qy 204 Db 232	Qy 24 TCCGCCCGTGTGGAGTGGGGGCCTGGGTGGGAATGGGCGTGTGCCAGCGCACGC 1	ORIGIN Query Match Best Local Similari Matches 918; Con	source 1994 /organism="Homo sapiens" /mol type="maxNA" /db_xref="taxon:9806" /clome="CSODCO15YH21" /clome="CSODCO15YH21" /clone_Tib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED" /clone_Tib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED" /note="left strand cDNA was primed with a NotI-oligo(dT)

γQ	D Qy	Db Qy	B &	ם מ			ORIGIN			FEATURES				AUTHORS TITLE JOURNAL COMMENT	ORGANISM REFERENCE	VERSION VERSION KEYWORDS SOURCE	BX353271/c LOCUS DEFINITION	Db RESULT 8	40	Qy da
1704 CTGGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGGATGTCTTCCGGCCTGGGGATG 1763	1644 CAGGTGAGCCAAGGGCTGCTGGTGGCCCCGGTAAGCCAAGCAGTCCCCATTCCTGGGCTATG 1703	1586 GATGTCACCACAGGAGAGCCAATTCGGGA-CCCCCAGGGGCACTGTATGGCCACATCT-C 1643	1526 GCIGIGGGGTGCTICCTGGCTTTACAAGCATATCTTCCCCTTCTCCTTGATTCGCTAT 1585 :	920 GAAACATATGRACTKACAGAGGGCAACGT-GCCACCTTCAACWACACAGGACAGCGGGGG	89 <u>1</u>	Watch 35.6%; Score 855; DB 13; Length 1200; Similarity 97.1%; Pred. No. 2.5e-135;	primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	/tissue_type="NEUROBLASTOMA_COT_25-NORMALIZED" /tissue_type="NEUROBLASTOMA_COT_25-NORMALIZED" /clone_lib="Homo sapiens NEUROBLASTOMA_COT_25-NORMALIZED" /note="1st_strand_cDNA_was_primed_with_a_NotI-oligo(dT)		708	<pre>http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSODC003CC09NPl&cluster=661.f. Contact :</pre>	Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 661.f For more information about this cluster, see	Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr	Li, W.B., G Full-lengt Unpublishe	Momo sapiens Eukaryota; Me Mammalia; Eut 1 (bases 1 t	JN BA33371.1 GI:30371745 BX353271.1 GI:30371745 3 EST. Homo sapiens (human)		949 CTGTGGGCTGCAGSCARO	923 CTGTGGGCTGCAGGCCCAGGAACCCACCCTGCTGGAATTAGCGATTT 969	863 CCAGAGTTTCTGGAGTCCCTGGAGCCGGACCTGCCCGCCC
		COMMENT	REFERENCE AUTHORS TITLE JOIRNAL	ORGANISM	VERSION KEYWORDS SOURCE	DEFINITION ACCESSION	RESULT 9 BQ680322 LOCUS	90	בר אל מיני	D D	Q B	Q	d dq	Qy	Qy	da	Q Qy	A dd	Db	ם סט סע
http://image.llnl.gov Plate: LLCM2333 row: m column: 04	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be	Contact: Robert Strausberg, Ph Contact: Robert Strausberg, Ph Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP Tissue Procurement: DCTD/DTP	1 (Dases 1 to 908) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unruphished (1999)			N AGENCOURT_8032839 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6091179 5', mENA sequence. 1 E0680312	mRNA	2364 IAAIRAAIGIGGCIGGAG 2381 : 21 TAATAAATGTGGMAGGAG 4			201 TAGGTGCCTACCTGACCACACTGCCCGGTACGGCGCCCTCCTGGCAGGAAACCTTC 142 2244 GAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGAG	TAGGTGCCTACCTGCCCCTCACAACTGCCCCGGTACAGCGCCCCTCCTGGCAGGAAACCTTC	2124 CAAATGAGGGCTTCGACCCCAGCACCCTGTCTGACCCACTGTACGTTCTGGACCAGGCTG 2183	2064 TCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAGTTCGGATGG 2123	2004 TTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCCACCCTTATGCCCGGCCCCGATTCC 2063	1944 GGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCCCCAGGCTTTGGACC 2003	AGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATGGAGTCACTGTGCCAG	1824 ATCGTACTGGAGACACCTTCAGGTGGAAGGGGGGAGAATGTGGCCCACAACCGAGGTGGCAG 1883	621 TTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAAGGTTTTCTCCGCTTCCATG 562	681 CTGGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGGATGTCTTCCCGGCCTGGGGATG 622 1764 TTTTCTTCAACACTGGGGAACCTGGTGGTCTGCGATGACCAAGGTTTTCTCCGCTTCCATG 1823

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 CCCTCCTGGCAGGAAACCTTCGAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGG 2282
                                                                   TGTACGTTCTGGACCAGGCTGTAGGTGCCTACCTGCCCCTCACAACTGCCCGGTACAGCG 2222
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Location/Qualifiers
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/lab host="NHH00B (phage resistant)"
/clone_lib="NIH MGC_112"
/clone_lib="NIH MGC_112"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ ade by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 661.f For
more information about this cluster, see
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On Feb 13, 2001 this sequence version replace
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 870)
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AL529216 Homo sapiens NEUROBLASTOMA COT 50-NORN CDNA Clone CSODD002YE03 3-PRIME, mRNA sequence
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1; Mismatches 3;
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                                                                                              Mammalla; Butheria; Primates; Catarrhini; Homin 1 (bases 1 to 934)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Prill-length cDNA libraries and normalization Unpublished (2001)

On Feb 13, 2001 this sequence version replaced Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 661.f
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODB001BC09QP1&cluster=661.f. Conta
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AL521330 AL521330 GI:31039633
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Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Faraday Avenue Genoscope sequence ID: CSODBO
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CGCGAGAGTAACAGGGCTGCACGCGCCTTCCTACGTGCGCTAGGCTGGGACTGGGGACCC
                           CGCGAGAGTAACAGGGCTGCACGCGCCCTTCCTACGTGCGCTAGGCTGGGACTGGGGACCC
                                                                                                                      CGCGCCGCACACCTTTCTCATTCACGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAG
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="CSODB001YE18"
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	Qy 1623 GGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGGTGGTGGCCCCGGTAAGCCAGC 1682		Qy 1503 TCAACTACACAGGACAGCGGGGGGCGTTGGGGGTTTCTGGCTTTACAAGCATATCT 1562	Query Match 32.7%; Score 786.8; DB 13; Length 903; Best Local Similarity 99.1%; Pred. No. 9.2e-124; Matches 791; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."	/lab_host="DH10B (phage-resistant)" /clone lib="NH MGC 112" /clone tib="NH MGC 112" /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. DIrectionally cloned into EcoRI/XhoI sites using the following 5' adaptor: into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California,	/organism="Homo sapiens" /mol_type="mRNA" /db xref="taxon:9606" /clone="IMAGE:6261109" /tissue type="melanotic melanoma, cell line"	1	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINIA) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP cDNA Library Preparation: Rubin Laboratory	REFERENCE 1 (Dases 1 to 903) AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999)	-	ION BQ678639 N BQ678639.1 G DS EST.	RESULT 12 BQ678639 BQ678	Db 906 TGGGTGCTGGCG-CARASTTTCTGGAGTCC 934	Oy 791 CCCACCGCCTGCGGCGGGGCCCCTGCTGCACTGCCCAGCTGCGGGGGGGG	
FEATURES Location/Qualifiers	<pre>ctp://www.genoscope.cns.ri/ cgi-bin/cluster.cgi?seq=CSODD002AC02QP1&cluster=661.f. Contact :</pre>	Email: segref@genoscope.cns.tr, Web : www.genoscope.cns.tr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 661.f For more information about the cluster, see	COMMENT On Feb 13, 2001 this sequence version replaced g1:12792710. Contact: Genoscope Centre National de Sequencage Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France	REFERENCE 1 (bases 1 to 873) AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D. TITLE Full-length cDNA libraries and normalization JOURNAL Unpublished (2001)	KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	N OΝ ω	Qy 2283 AACTCTGTGGGGTGGGG 2300 	Qy 2223 CCCTCCTGGCAGGAAACCTTCGAGAACTTCCACACCTGAGGCACGCGAGAGAGG 2282	Qy 2163 TGTACGTTCTGGACCAGGCTGTAGGTGCCCTACCTGCCCCTCACAACTGCCCGGTACAGCG 2222	OY 2103 AACAGCAGAAAGTTCGGATGGCAAATGAGGGCTTCGACCCCAGCACCCTGTCTGACCCAC 2162	Qy 2043 CTTATGCCCGGGCCCCGATTCCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCA 2102	Qy 1983 GTCCCCCCACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCCAC 2042	Qy 1923 TCTATGGAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGC 1982	192 420		Db 181 AGTCCCCATTCCTGGGCTATGCTGGCGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGG 240 Qy 1743 ATGTCTTCCGGCCTGGGGATGTTTTCTTCAACACTGGGGACCTGGTGGTGGGATGACC 1802	

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODD002YE03"
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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLAM11443 row: g column: 20
High quality sequence stop: 789.
                                                                                                                                                         122 CTAGGTTTTCGGAAGGGAGGATCAGGGATGTTTGCGAGCGGCTGGAACCAGACGGTGCCG
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone lib="WIH MGC 115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: ECORV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5177899"
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Pred. No. 2.1e-120;
0; Mismatches 58;
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : filang@lifetech.com |
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF017AE04QP1.
Location/Qualifiers
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BX419446 Homo sapiens FETAL BRAIN Homo sapiens cDNA
CSODF017YI07 5-PRIME, mRNA sequence.
                                                                                                                                                                                              Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; (bases 1 to 969)
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/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
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Pred. No. 4.2e-118;
3; Mismatches 2;
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Search completed: July 3, 2004, 03:46:26
Job time: 6117 secs

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   GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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ABX9236099
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ADA12301
ADC129106
ADB763323
ADC43749
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Aaf27417 Human fat
Ada84114 Human POM
Aad49501 Human TRI
Aaf89054 Human FAT
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ALIGNMENTS

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18-OCT-1999; 99US-0159586P
25-APR-2000; 2000JP-00128993
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The invention relates to a novel human fatty acid transporter, PSEC67 (AAB60388), and to cDNA encoding it (AAF27417). PSEC67 is responsible for the uptake of oleic acid into cells. The invention also relates to vectors and host cells comprising a PSEC67 nucleic acid; the recombinant production of PSEC67; an antibody against PSEC67; methods of screening for compounds which can regulate the uptake of long-chain fatty acids into cells; and the compounds thus identified. The PSEC67 protein and the

the

for

Fatty acid transporter protein and encoded gene PSEC67 cloned from human cDNA library, with activity of oleic acid incorporation, useful as target molecule of preventives or remedies of fatty-acid metabolic disorders.

P-PSDB;

Claim

1; Page 44-48; 58pp; Japanese.

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Determining if a nucleic acid is a marker for a phenotype/ceil type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all ESTs expressed in normal tissue. Claim 23; Page 490-491; 516pp; English. The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a	0-MAY-2001; 2001US-0293999P. 2-CCT-2001; 2001US-0330457P. 9-FEB-2002; 2002US-0357144P. BIOM-) BIOMEDICAL CENT. aranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL PSDB; ADA84115.	OM124 ge marker; induced; ds; ge piens. 03028-A2 2002; 20	2401 CCTAC 2405	ACTGTACGTTCTGGACCAGGTGTAGGTGCTACCTGCCCCTCACAACTGCCCGGTACAG 222	1981 GCGTCCCCCCCACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCC 2040 2041 ACCTTATGCCCGGCCCCGATTCCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGAGCCTT 2100
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	421 GGCCAGCAGCAGCCGCACACCTTTCTAATTAACGCTCGCGGCCTTTTAGCTACTC 480 [ĠŔĬŔĠŔĠŔŔĠĠĠĊŦĊĊŔĬĠĠĊĬĠĊĠĠĊĠĊĠĊĠĊĠĊĠĊĠĊĊĠĠŦĠĊĊĊŦĠĊŦĠĊŦĠĊŦĠĊŦĠĊ	8 GCACTCCTCCGGGGTTTCTGCTTCCGCCCGTGGAAGGAGAAGTCTAGAACGAGCGGC 120 61 GGGCGTGTGCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGC 120 68 GGGCGTGTGCCAGCGCACGCCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGC 127 121 CCTAGGTTTTCGGAAGGAGGATCAGGGAGTTTTGCGAACCAGACCAGACGGTGCC 180 11	phenotype such as hyperosmotic stress or high salt conditions. A method of the invention is also useful for determining the progression of colon cancer in a human, for detecting a tumour cell, and for regulating or preventing the growth of a tumour cell. An antibody of the invention is useful for detecting the absence or presence of peptides encoded by tumour-associated markers. A polypeptide of the invention is useful as an immunogen for vaccinating an animal. The present sequence encodes a tumour-associated marigen of the invention. X Sequence 2430 BP; 430 A; 740 C; 781 G; 479 T; 0 U; 0 Other; Ouery Match Dest Local Similarity 100.0%; Score 2405; DB 7; Length 2430; Matches 2405; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 2405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	biological species. The method comprises performing a global comparison of a group of expressed sequence tags (ESTs) known to be expressed in the phenotype/cell type of interest with all ESTs expressed in normal tissue in order to identify ESTs that are preferentially expressed in the phenotype/cell of interest. A method of the invention is useful for determining whether a nucleic acid is a marker for a predetermined phenotype or cell type of interest from a biological species, preferably as a tress or human. The cell type of interest is an abnormal cell such as a tress-induced

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25-MAY-2001;
22-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human transporters and ion channels (TRICH) polypeptides and nucleic acid molecules encoding such polypeptides. proteins are useful for preparing compositions for diagnosing or tre diseases or conditions associated with decreased expression or overexpression of functional TRICH e.g. atherosclerosis or cancer. The present sequence is human Trucker invention is useful in gene therapy. The present sequence is human Trucker.
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Tang YT, Yue H, Raumann BE, Lal PG, Azimz:
Thornton M, Nguyen DB, Arvizu CS, Emerling
Thornton M, Nguyen DB, Arvizu CS, Emerling
J, Ding L, He A, Griffin JA, Sanjanwala MM;
Xu Y, Au-Young JK, Das D, Lee SY, Chang J
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                                                                                    transport protein; FATP; human; mouse; rat; rice blast fungus; absorption; obesity; diabetes; heart disease; hyperlipidaemia;
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                                                                       tuberculosis;
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Best Local
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23-SEP-1999;
16-DEC-1999;
17-FEB-2000;
06-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New fatty acid transport proteins (FATPs) useful for the manufacture medicament for treating obesity, diabetes and heart disease.
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AGCGCGCGCACACCTTTCTCATTCACGGCTCGCGGGCGTTTAGCTACTCAGAGGCGG
                                                                    ACCCGGAAGGTCCCGAGGGGGGGCTGCAGCCTGGCCTTGGCGCAACTGGCCCAGC
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99US-00465280.
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GCGGTCACTATTTTGTAATAATGTGGCTGGAGCTGATCCAGCTGTCTCTGA
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AAZ33977 standard; cDNA; 2574 ₿P.

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Human PRO703 nucleotide sequence.

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ID AAZ3
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AC AAZ2
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DT 07-L
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KW Huma
KW Brob
KW Bect
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OS Homc Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein; ss.

Homo sapiens

WO9946281-A2

10-MAR-1998; 11-MAR-1998; 11-MAR-1998;

99WO-US005028

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98US-0077791P

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98US-007804P

98US-007886P

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New secreted and trauseful for treating adhesion disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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P-PSDB; AAY41699.
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                                                                                                                                        AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide provide specific targeting of bioactive molecules to cells. AAC786987 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences
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Baker KP, Wood WI; Baker Desauvage Ξ Goddard A, Gurney AL, Klein RD, Roy MA:

WPI; 2000-572269/53. P-PSDB; AAB24054.

New isolated antibody for use in compositions and methods for the diagnosis and treatment of neoplastic cell growth and proliferation mammals, including humans, and in monitoring tumor treatment.

Claim 50; Fig 28; 195pp; English.

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The present invention describes an isolated antibody (Ab) that binds to one of the human proteins (P) designated PRO213, PRO1330, PRO1449, PRO377, PRO324, PRO351, PRO362, PRO615, PRO531, PRO538, PRO3644 PRO518, PRO772, PRO773, PRO792 or PRO474. The Ab can be used in compositions and methods for the diagnosis and treatment of neoplastic cell growth and proliferation in mammals, including humans. Genes and polypeptides encoded by them, that are amplified in the genome of a tumour cell, can be identified and are useful targets for the treatment and prevention of certain cancers and may be used to monitor tumour treatment. Compounds that inhibit the expression or activity of the identified polypeptides can be identified and used as antagonists. Benign or malignant tumours, inflammatory disorders and immunological disorders can be treated. and

794 TICTGTGGCTCTGGTTCGGCCTAAGGCCGCCTGCGCACTGCCTTTGTGCCCACCG 798 CCCTGCGCCGGGGCCCCTGCTGCACTGCCTCCGCACTGCGCGCGC	CGCCCGAAGCGGCCCGAGTTTGCCCGAGGGGACGGTGCCCCCAGAGGTGCCCCCAGAGGTGCCCCCAGAGGTGCCCCCAGAGGTGCCCCCCGCAGAGGTGCCCCCCCGCTGGAGCAACTGTGGCCCCCCCC	Db 554 GTAACAGGGCGCCTTCACGTACGTACGTACGTACGTACGT		374 IGIGCIGHAMAGGGCICTICGAGCICGCGCCCGCGCAAC 378 GICCCGAGGGGGGCTGCAGCCTGGCCTGGCGCAAC		198 CCATGGCTGCCTCCTGCTGCCCCCTGCTGCTGCTGCTGCTGCT	QY 138 GAGGATCAGGGATGTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGCGGGCT 19	78 CGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGCCCCTAGGTTTTCGGAAGG	TREETS (TREETS	Query Match 99.3%; Score 2387; DB 3; Length 2574; Best Local Similarity 100.0%; Pred. No. 0; Marches 2387: Conservative 0: Miamatches 0: Indels 0: Gan	CC AAC58123 to AAC58224 represent hybridiation probes and PCR primers used CC in the isolation of the human PRO sequences. AAC58225 to AAC58241 and CC AAB24041 to AAB34056 represent human PRO polynucleotide and protein CC sequences given in the exemplification of the present invention XX SQ Sequence 2574 BP; 470 A; 775 C; 821 G; 508 T; 0 U; 0 Other;
CÓATGATCGTACTGGAGACACCTTCAGGTGGAGGGGAGAATGTGGCCACGGGAGAGAGTCTTCGAGGGGGAGAGATGTGGGCCACGGGAGAGATGTTCTTCAGGAGGGGAGAATGTGGGCCACGGGGAGAGGTGAACGTCTATGCGGCAGAGGTCTTCGAGGAGGTGAACGTCTATGCGCAGAGAGGTCTTCGAGGAGGCCTAGGTCTCTCAGGAGGCAGGC	Db 1754 GCTATGCTGGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGGATGTCTTCCGGCCTG 1813 Qy 1758 GGGATGTTTCTTCAACACTGGGGACCTGGTCTGCGATGACCAAGGTTTTCTCCCGCT 1817	Qy 1638 CATCTCCAGGTGAGCCAGGGGTGGTGGCCCCGGTAAGCCAGCAGTCCTGG 1697	1578 TTCGCTATGATGTCACCACAGGAGAGCCCAATTCGGGACCCCTAGGGCA 1	1458 AGGTGCTGGAGACATATGGACTGACAGAGGGCAACGTGGCCACCATCAACTACACAGGAC	Db 1394 GATACCTTGTCAACCLAICTAGCCCCAGACAAGGCAGAAGGCAGAAGGCAGCAGCTGCGCAGCTAGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	Qy 1278 TCTGGGAAGATTGCCAGCACGAGGATGACGTGTCCAGTACATTGGGGAGCTGTGCC 1337	1218 TEGGCTGCARTGGGCCACAGTGGTGCTGAAATCCAAGTTCTCGGCTGGTCAGT	58 AAGATGTGATCTACCTCGCCCTCCCACTCTACCACATGTCCGGTTCCCTGCTGGGCATCG	Qy 1098 TCAGTCATCTGAAGATCCTGCAATGCCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGG 1157	Qy 1038 CAGACACGTGCCTGTACATCTTCACCTCTGGCACCACGGGCCTCCCCAAGGCTGCTCGGA 1097	Db 974 TCCACCTGTGGGCTGCAGGCCCAGGAACCCACCCTGCTGGAATTAGCGATTTGCTGGCTG

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ndard; cDNA; 2574 BP. (first entry) secreted and transmembrane protein PRO703 cDNA. ted and transmembrane protein; PRO; virucide; gene therapy; growth induction cascade; blood coagulation cascade; ion; gene; ss. -Al. -Al. 2001US-00978191. 97US-00663449P. 97US-0066344P. 98US-0077450P. 98US-0077450P. 98US-0077641P. 98US-0077641P. 98US-0077649P. 98US-0077649P. 98US-0077649P. 98US-0077649P. 98US-0077649P. 98US-0077649P. 98US-0077649P. 98US-0077699P. 98US-0079804P. 98US-007966P.	CCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAGTTC
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(first entry)

human secreted and transmembrane protein PRO703

Human; secreted and transmembrane protein; PRO; antiinflammatory; antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytost antidiabetic; gene therapy; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; cancer; diabetic complication; chromosome megene mapping; pharmaceutical; diagnostic; biosensor; bioreactor; tissue typing; gene; ss. cytostatic; mapping;

sapiens

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99WC-US028565
99WC-US031274
2000WC-US031274
2000WC-US00376
2000WC-US003454
2000WC-US005841
                       2001WO-US017800.
2001WO-US019692.
2001WO-US021066.
2001WO-US021735.
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98US-0081817P
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98WO-US021141.
98WO-US024855.
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Ashkenazi AJ, Baker KP, Botstein I Ferrara N, Filvaroff E, Fong S, (Goddard A, Godowski PJ, Grimaldi Kljavin IJ, Kuo SS, Napier MA, P, Stewart TA, Tumas D, Williams PM, Botstein D, Desnoyers L, Eaton DL; Fong S, Gao W, Gerber H, Gerritsen ME; Grimaldi JC, Gurney AL, Hillan KJ; ier MA, Pan J, Paoni NF, Roy MA, Shelt. lliams PM, Wood WI; Shelton 멅

WPI; 2003-328860/31. P-PSDB; ABU72207.

New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or

Claim 2; Fig 38; 453pp; English

The invention describes an isolated nucleic acid (1) comprising, or which is at least 80 % sequence identity to, or the full-length coding sequence of, any of 118 300-2100 nucleotide sequences, which encodes its corresponding PRO polypeptide selected from 118 100-700 amino acid sequences, all given in the specification. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, or diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreaccors. Both are useful in tissue typing. This sequence encodes a novel human secreted and transmembrane PRO polypeptide

Sequence 2574 BP; 470 A; 775 C; 821 <u>ი</u> 508 T; 0 U; 0

Matches 2387; Query Match Best Local :

Similarity

99.3%;

Score 2387; Pred. No. 0;

В 7;

Length 2574;

Conservative

Ś S 밁 Ş 밁 Ş 뭐 Š 맑 Š 밁 S 문 Ś В Ś В Ś 498 494 438 434 378 374 318 314 258 254 198 194 138 GAGGATCAGGGATGTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAGAGAGGAAGCCGGCCT 134 78 74 18 GTAACAGGGCTGCACGCCCTTCCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGGCG GCGACAGCGGCGAGGGGGCGCTGGAGAAGGCGAGCGGGGCGCCGGGGAGCCCGGAGATG GTAACAGGGCTGCACGCGCTTCCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGGCG CGCACACCTTTCTCATTCACGGCTCGCGGGCGCTTTAGCTACAGAGGCGGGAGCGCGAGA GTCCCGAGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAACTGGCCCAGCAGCGCGCCG GTCCCGAGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAACTGGCCCAGCAGCGCCCCG TACACCTCTGGCCGCAGTTGCGCTGGCTTCCGGCGGACTTGGGCCTTTGCGGTGCGAGCTC GAGGATCAGGGATGTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGCGGGCT CGCACACCTTTCTCATTCACGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGA тепестесьмым вестсттеннего в пответственнего в по TACACCTCTGGCCGCAGTTGCGCTTGGCCTTCCGGCGACTTGGCCCTTTGCGGTGCGAGCTC CCATGGCTGCCTGCTGCTGCCCCCTGCTGCTGCTACCGCTGCTGCTGCTGAAGC CCATGGCTGCCTCCTGCTGCCCCCTGCTGCTTGCTACCGCTGCTGCTGCTGAAGC CGCGCGCTCCCTGGAAGGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTTCGGAAGG CGCGCGCTCCCTGGAAGGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTTCCGGAAGG CTGCTCTCCGCCCGTGTGGAGTGGTGGGGGCCTGGGGAATGGGCGTGTGCCAGCGCA crecrerececereresereseresecereseresearesecereresecereseere 0 Mismatches 0 Indels 0 Gaps 613 557 437 493 373 317 313 197 193 137 133 257 253 77

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	638 CATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCAGCAGTCCCCCATTCCTGG 1697	578 TICGCTATGATGICACCACAGGAGAGCCAATICGGGACCCCCAGGGGCACTGTATGGCCA 1637	518 AGCGGGGCCTGTGGGCGTGCTTCCTGGCTTTACAAGCATATCTTCCCCTTCTCCTTGA 1577	458 AGGTGCTGGAGACATATGGACTGACAGAGGGCAACGTGGCCACCATCAACTACACAGGAC 1517	398 TGGGCAGCGGGCTGCGCCCAGATACCTGGGAGCGTTTTGTGCGGCGCTTCGGGCCCCTGC 1457	338 GATACCTTGTCAACCAGCCCCCGAGCAAGGCAGAACGTGGCCATAAGGTCCGGCTGGCAG 1397	278 TCTGGGAAGATTGCCAGCAGCAGCAGGGTGACGGTGTTCCAGTACATTGGGGAGCTGTGCC 1337	218 TGGGCTGCATGGGCATTGGGGCCACAGTGGTGCTGAAATCCAAGTTCTCGGCTGGTCAGT 1277	158 AAGATGTGATCTACCTCGCCCTCCCACTCTACCACATGTCCGGTTCCCTGCTGGGGATCG 1217	098 TCAGTCATCTGAAGATCCTGCAATGCCAGGGCTTCTATCAGCTGTGTGTG	038 CAGACACGTGCCTGTACATCTTCACCTCTGGCACCACGGGCCTCCCCAAGGCTGCTCGGA 1097	978 AAGTGTCCGCTGAAGTGGATGGGCCAGTGCCAGGATACCTCTCTTCCCCCCAGAGCATAA 1037	918 TCCACCIGTGGGCTGCAGGCCCAGGAACCCACCCTGCTGGAATTAGCGATTIGCTGGCTG 977	858 TGGCGCCAGAGTTTCTGGAGTCCCTGGAGCCGGACCTGCCCGCCC	798 CCCTGCGCCGGGGCCCCCTGCTGCACTGCCTCCGCAGCTGCGGCGCGCGC	738 TICTGIGGETCIGGETIGGGGCTGGCCAAGGCCGGCCTGCGCACTGCCTTTGIGCCCACCG 797	678 CCGCCGCCCTCTGTCACCTGGAGCAACTGTGGGCGCTGCTCCTCCCCGCTGGCCCAGAGT 737	618 CAGCGGCCGGAAGCGGCGCGGAGTTTGCCGGAGGGGACGGTGCCGCCAGAGGTGGAGGAG 677	
5	OS Homo sapiens.	KW glomerulonephritis; lung disease; pulmonary l KW bronchial asthma; gastric ulcer; renal failu KW inflammatory bowel disease; reproductive dise	KW apoptosis related condition; AIDS; amyotrophi KW inflammatory disease, asthma; atherosclerosis KW gastrointestinal discorder; Alzheimer's disease KW hypertension; myocardial ischaemia; kidney di	DE Human secreted and transmembrane polypeptide XX XW Human; ss; gene; thrombolytic agent; interfe; KW erythropoletin; colony stimulating factor; co	AC ACA71709; XX DT 11-AUG-2003 (first entry)	RESULT 10 ACA71709 ID ACA71709 standard; cDNA; 2574 BP. XX	Db 2414 ATTTTGTAATAAATGTGGCTGGAGCTGATCCAGCTC	2354 GGGCCGTI	ACCITCGA ACCITCGA B GGGCCGTT	2234 AGGCTGTA	2174 GGATGGCA	2114 GATTCCTC	2054 TGGACCTT	94 TGGACCTT	1934 TGGCAGAG	1878 TGGCAGAG	1/58 GGATGTT	1754 GCTATGCT	1694 CATCTC

AGAGACCTTCAAACAGCAGAAAGTTC GGGGGAGAATGTGGCCACAACCGAGG GTTGCTAAAGGATGTCTTCCGGCCTG TGTCTCTGACCTA 2404 rtrictataccagaacticcicicact TTTTCTATACCAGAACTGCGGTCACT STCTGACCCACTGTACGTTCTGGACC STCTGACCCACTGTACGTTCTGGACC BAACTTGCCACCTTATGCCCGGCCCC CCTAGTTCTGCGTCCCCCCCCACGCTT GAGGTGAACGTCTATGGAGTCACTG CIGCGAIGACCAAGGITITCTCCGCT strectaaaggatgtetteggeetg GTAAGCCAGCAGTCCCCATTCCTGG PGTCTCTGACCTA 2460 CGGTACAGCGCCCTCCTGGCAGGAA BAACTTGCCACCTTATGCCCGGCCCC GAGGTGAACGTCTATGGAGTCACTG CTGAGAGAGGAACTCTGTGGGGTGG CTGAGAGAGGAACTCTGTGGGGTGG CGGTACAGCGCCCTCCTGGCAGGAA 1817 1813 1757 1753 2113 2057 2297 2293 2237 2233 2173 2117 1997 1993 1933 2413 2357 2353 2177 2053 1937 1877 1873

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PRO703 cDNA.

rferon; interleukin; cytokine; cancer; colorectal carcinoma; ophic lateral sclerosis; osis; neurodegenerative disease; sease; Parkinson's disease; y disease; carcinogenesis; ry hypertension; preeclampsia; ry hypertension; preeclampsia; ilure; cardiovascular disease; disorder; premature labour.

US2002177553-A1.

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12.MAR-1999;
112.APR-1999;
114.MAY-1999;
125.AUG-1999;
25.AUG-1999;
25.AUG-1999;
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28-FEB-2001
22-MAR-2001
22-MAR-2001
22-MAR-2001
10-MAY-2001
10-MAY-2001
10-JUN-2001
01-JUN-2001
11-JUN-2001
2000US-0079238.
2000US-US032678.
2000WC-US032678.
2000WC-US034959.
2000WC-US034959.
2001WC-US006520.
2001US-00816744.
2001US-00816920.
2001US-00854200.
2001US-00854200.
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2001US-0085436.
2001US-00886346.
2001US-00886346.
2001US-0US0196932.
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2001US-0US0196932.
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(GETH) GENENTECH INC.

Ashkenazi AJ Ferrara N, Goddard A, Kljavin IJ, Stewart TA, Æ, WJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Pilvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ; KWO SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelt-Tumas D, Williams PM, Wood WI; Shelton DL;

WPI; 2003-328499/31. P-PSDB; ABU84887.

New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying modulators of receptor-ligand interactions.

Claim 2; SEQ ID NO 101; 55pp; English.

CC The invention relates to an isolated secreted and transmembrane CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful CC in PRO polypeptide detection methods. The PRO polypeptide is useful for CC inking a bioactive molecule to a cell. The PRO polypeptide or an accordance of the PRO polypeptide or an accordance of the PRO polypeptide or an accordance of the PRO polypeptide is useful for modulating a biological activity of a cell. The PRO polypeptide is useful in industrial applications including pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO polypeptide is useful in industrial applications including CC pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO polypeptide is useful for treating disease such as cytokines. The PRO polypeptide is useful for treating disease such as concer e.g. colorectal carcinoma, apoptosis related conditions e.g. AIDS, CC amystrophic lateral sclerosis; inflammatory disease e.g. asthma, cC amystrophic lateral sclerosis; inflammatory disease e.g. Alzheimer's disease, CC amystrophic lateral sclerosis; inflammatory disease e.g. hypertension and CC myocardial ischaemia; kidney disease e.g. renal failure and CC parkinson's disease; cardiovascular disease e.g. hypertension, bronchial asthma, gastrointestinal disorders e.g. gastric ulcer and inflammatory companies and carcinogenesis. The present sequence represents a cDNA central polypeptide of the invention. Note: The sequence data for chis patent did not form part of the printed specification but was cobalance in electronic format directly from USPTO at

Sequence 470 A Ç. 821 <u>ი</u> 508 Ŧ, 0 u; o

Query Match 99.3%; Best Local Similarity 100.0%; Matches 2387; Conservative

Score 2387; D); Pred. No. 0; O; Mismatches

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2174 GGATGGCAAATGGGGGCTTCGACCCCGACGACCCGGTACAGGGCCTCCTGGCAGGACCCTGTAGGGGCTTCTGACCCGTGTAGGGGCTTCTGACCACGACGGGCCTCCACAACTGCCGGGAACTGCCGGGAACTGCCGGGAACTGCCCGGTACAGGGCCTCCTGGCAGGAACTGCCCGGTACAGCGCCTCCTGGCAGGAACTGCCCGGTACAGCGCCTCCTGGCAGGAACTGCCCGGTACAGCGCCCTCCTGGCAGGAACTGCCCGGTACAGGCACCTCCTGGCAGGAACTCTGCACAGGAACTCTGAGGGAACTCTGTGGGGGTACAGCTGAGGAGAACTCTGTGGGGGTGGGT	2058 GATTCCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAGTTC	1994 TGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCCCCC	1938 TGCCAGGCATGAAGGCAGGGCTGGAATGTCTTCAGGAGGTGTACGCCCCCCCC	818 874	58 14	1698 GCTATGCTGGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGGATGTCTTCCGGCCTG	1638 CATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCGGTAAGCCAGCAGTCCCCATTCCTGG	1578 TTCGCTATGATGTCACCACAGGAGAGCCAATTCGGGACCCCCAGGGGCACTGTATGGCCA	18 74	1458 AGGTGCTGGACACATATGGACTGACAAAGGCAACGTGGCCACCATCAACTACACAGGACACGACGACGACGACGACGACATCAACTACACAGAGACGACATGACACGACAACGACGACATCAACTACACAGACAG	00 44	9 8 9 4	1278 TCTGGGAAGATTGCCAGCAGCACAGGGTGACGGTGTTCCAGTACATTGGGGAGCTGTGC	1218 TGGGCTGCATGGGCAFTGGGGCCACAGTGGTGCTGAAATCCAAGTTCTCGGCTGGTCAGT	14

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17-OCT-1997;
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    Ashkenazi A,
Ferrara N,
Goddard A,
Kljavin IJ,
Stewart TA,
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11.-MAR-1999
12.-APR-1999
12.-APR-1999
22.-AUG-1999
25.-AUG-1999
25.-AUG-1999
25.-AUG-1999
26.-DEC-1999
27.-DEC-1999
27.-DEC-1999
27.-DEC-1999
27.-DEC-1999
27.-MAR-2000
27.-MAR-2001
The present invention relates to the polypeptides, and the polynucleotide polypeptides are secreted and transme
                                                                                                                          Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating cancer, kidney diseases, bone, cartilage disorders and immune deficiencies.
                                                                                    Claim
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DB; ABU61085.
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Filvaroff E,
Godowski PJ,
Kuo SS, Nap,
Tumas D, Wi
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99US-00205190
99US-00208191
99US-00311832
99WO-US012252
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99WO-US012551
99WO-US028551
99WO-US028551
99WO-US031274
2900WO-US031274
2000WO-US030277
2000WO-US030565
2000WO-US030565
2000WO-US0305641
2000WO-US03565
2000WO-US0356520
2000WO-US034441
2000WO-US034459
2000WO-US0346784
2000WO-US034678
2000WO-US03478
2000WO
                                                                                    38;
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                                                                                                                                                                                                                                                                        KP, Botstein D, Desnoyers L, Eaton D;
E E, Fong S, Gao W, Gerber H, Gerrisen ME;
PJ, Grimaldi JC, Gurney AL, Hillan KJ;
Napier MA, Pan J, Paoni NF, Roy MA, Shelton, Williams PM, Wood WI;
                                                                               English.
    to the isolation of novel human leotide sequences encoding them. transmembrane proteins. The PRO
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PRC

79	678 CCGCCCCCCTCTGTCACCTGGAGCAACTGTGGCGCTGCTCCCCCGCTGGCCCAGAGT 737	618 CAGCGGCCGGAAGCGGCGCGGAGTTTGCCGGAGGGGACGGTGCCGCCAGAGGTGGAGGAG 677	558 GCGACAGCGGCGAGGGGAGCCGTCGAGAAGGCGAGCGGGCAGCCGGGAGATG 617			378 GICCCGAGGGGGCTGCAGCCTGGCCTCGCCGCAACTGGCCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	318 TGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGGGCTGCCGCCGGACCCGGAAG 377	258 TACACCTCTGGCCGCAGTTGCGCTGGCTTCCGGCGGACTTGGCCTTTGCGGTGCGAGCTC 317	198 CCATGGCTGCCTCCTGCTGCCCCCTGCTGCTGCTACCGCTGCTGCTGCTGAAGC 257	138 GAGGATCAGGGATGTTTGCGAGCGGGCTGGAACCAGACGGTGCCGATAGAGGAAGCAGCGGCT 197	78 CGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTTCGGAAGG 137	18 CTGCTCTCCGCCCGTGTGGAGTGGGGGGCCTGGGTGGGAATGGGCGTGTGCCAGCGCA 77	Query Match 99.3%; Score 2387; DB 7; Length 2574; Best Local Similarity 100.0%; Pred. No. 0; Matches 2387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	segdata.uspto.gov/psipsDIDEntry.html Sequence 2574 BP; 470 A; 775 C; 821 G; 508 T; 0 U; 0 Other;	animals, for the generic analysis of individuals with genetic disorders, and in gene therapy. The present sequence encodes a human PRO polypeptide of the invention. Note: The sequence data for this patent was obtained in	disorders, kidney disorders, bone and cartilage disorders or arthritis, tumours, and wound healing. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation	identifying agonists or antagonists. The bloactive molecule maybe a toxin, radiolabel or antibody, and causes apoptosis or death of the cell. The PRO polypeptides are useful for treating immune disorders, diabetes or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system	polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, for modulating biological activities of cells expressing PRO polypeptides, and for for
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1818 TCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGCCCACAACCGAGG	L/58 GGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAAGGTTTTCTCCGCT 1817 LB14 GGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAAGGTTTTCTCCCGCT 1873	698 GCTATGCTGGCGGGCCAGAGCTGGCCCAGGGAAGTTGCTAAAGGATGCTTCCGGCCTG :	CATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCAGCAGTCCCCATTCCTGG 1	8 TTCGCTATGATGTCACCACAGGAGAGCCCAATTCGGGACCCCCAGGGGCACTGTATGGCCA 1	1518 AGCGGGGCGCTGTGGGGCGTGCTTCCTGGCTTTACAAGCATATCTTCCCCTTCTCCCTTGA 1577	1458 AGGTGCTGGAGACATATGGACTGACAGAGGGCAACGTGGCCACCATCAACTACACAGGAC 1517 	1398 TGGGCAGCGGCTGCGCCCAGATACCTGGGAGCGTTTTGTGCGGCGCCTTCGGGCCCCTGC 1457	1338 GATACCTTGTCAACCAGCCCCCGAGCAAGGCAGACGTGGCCATAAGGTCCGGCTGGCAG 1397 	TCTGGGAAGATTGCCAGCAGCACAGGGTGACGGTGTTCCAGTACATTGGGGAGCTGTGCC 1	1218 TGGCCTGCATGGCCATTGGGCCACAGTGGTGCTGAAATCCAAGTTCTCGGCTGGTCAGT 1277	AGATETGATCTACCTCGCCCTCCCACTCTACCACATGTCCGGTTCCCTGCTGGGCATCG	8 TCAGTCATCTGAAGATCCTGCAATGCCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGG 1	8 CAGACACTGCCTGTACATCTTCACCTCTGGCACCACGGCCTCCCCAAGGCTGCTCGGA 1	8 AAGTGTCCGCTGAAGTGGATGGGCCAGTGCCAGAATACCTCTCCTCCCCCAGAGCATAA 1	TCCACCTGTGGGCTGCAGGCCCAGGAACCCACCTGCTGGAATTAGCGATTTGCTGGCTG	8 TGGCGCCAGAGTTTCTGGAGTCCCTGGAGCCGGACCTGCCCGCCC	798 CCCTGCGCCGGGGCCCCTGCTGCACTGCCTCCGCAGCTGCGGCGCGCGC	

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RESULT 12
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17-OCT-1997;
03-NOV-1997;
13-NOV-1997;
21-NOV-1997;
10-MAR-1998;
11-MAR-1998;
11-MAR-1998;
11-MAR-1998;
12-MAR-1998;
                                                                                                                                                                                                                                                                           Human; ss; gene; secreted protein; transmembrane protein; PRO; malignancy; cancer; ovarian cancer; colorectal cancer; sarcoma; leukaemia; lymphoma; inflammatory disease; necrosis; atherosclerosis; infertility; premature aging; psoriasis; inflammatory disease; renal disease; arthritis; immune-mediated alopecia; stroke; encephalitis; hepatitis; multiple sclerosis; gene therapy.
                                                                                                                                                                                                                                                    Homo
                                                                                                                                                         15-OCT-2001;
                                                                                                                                                                                       02-JAN-2003.
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   3-0066364P.
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29-MAR-1999;
21-MAR-2000;
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99US-00267213
99US-0031141
2000WO-US0013141
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2000WS-US0014941
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Best Local Sim
Matches 2387;
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05-JUN-2001;
14-JUN-2001;
19-JUN-2001;
29-JUN-2001;
29-JUN-2001;
09-JUL-2001;
30-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New genes and secreted and transmembrane polypeptides (e.g. PRO337 PRO1559), useful for treating or diagnosing e.g. cancers, atherosclerosis, infertility, stroke, encephalitis, hepatitis or musclerosis in mammals.
                                                                                                                                                                                            Sequence
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N, Filvaroff E,
A, Godowski PJ,
IJ, Kuo SS, Napi
TA, Tumas D, Wil
                                    CGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTTCGGAAGG
                                                                                                  CTGCTCTCCGCCGTGTGGAGTGGTGGGGGGCCCTGGGGTGGGAATGGGCGTGTGCCAGCGCA
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2001US-00874503.

2001US-0088263-

2001US-00886342.

2001WO-US019692.

2001WO-US021066.

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2001US-00918585.
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ilarity 100.0%;
Conservative
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E, Fong S, Gao W, Gerber H, Gerritsen ME;
PJ, Grimaldi JC, Gurney AL, Hillan KJ;
Napier MA, Pan J, Paoni NF, Roy MA, Shelt
Williams PM, Wood WI;
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                                                                                                                                   Score 2387; DI
Pred. No. 0;
0; Mismatches
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                 CAGCTAGAACGAGCGGCCCTAGGTTTTCGGAAGG
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                              AAGATGTGATCTACCTCGCCCTCCCACTCTACCACATGTCCGGTTCCCTGCTGGGCATCG
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R-1998; R-1998;	PR PR	2298 GGGCCGTTGCAGGTGTACTGGGCTGTCAGGGATCTTTTCTATACCAGAACTGCGGTCACT 2357
Ř-1998; R-1998; -1998;	סי _י סיס גע גע גע	2238 ACCTTCGAATCTGAGAACTTCCACACCTGAGAGCACCTGAGAGAGGAACTCTGTGGGGTGG 2297
x - 1998; x - 1998; x - 1998; x - 1998;	ਸ ਸ ਸ ਸ ਸ ਸ ਸ ਸ ਸ ਸ ਸ ਸ ਸ ਸ ਸ ਸ ਸ ਸ ਸ	2178 AGGCTGTAGGTGCCTACCTGCCCCTCACAACTGCCCGGTACAGCGCCCTCCTGGCAGGAA 2237
йй-1998; -1998; -1998;	ਸ਼ਕ ਸ਼ਕ੍ਰ ਸ਼ਕ੍ਰ	2118 GGATGGCAAATGAGGGCTTCGACCCCAGCACCCTGTCTGACCCACTGTACGTTCTGGACC 2177
RR-1998;	PR PR PR	2058 GATTCCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAGTTC 2117
R-1998; R-1998; R-1998;	אק אק אק	1998 TGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCCACCTTATGCCCGGCCCC 2057
R-1998; R-1998; R-1998;	98 8 8 8 8 8	1938 TGCCAGGGCATGAAGGCAGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCCCCC
R-1998; R-1998; R-1998; R-1998;	אַק אַק אַק	1878 TGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATGGAGTCACTG 1937
R-1998; R-1998; R-1998;	ਸ਼੍ਰ ਸ਼੍ਰ ਸ਼੍ਰ	1818 TOCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAAATGTGGCCACAACGGAGG 1877
21-NOV-1997, 97US-0066364P. 10-MAR-1998, 98US-0077450P. 11-MAR-1998, 98US-0077632P. 11-MAR-1998, 98US-0077641P.	ਸ ਸ਼੍ਰ ਸ਼੍ਰ ਸ਼੍ਰ ਸ਼੍ਰ ਸ਼੍ਰ ਸ਼੍ਰ ਸ਼੍ਰ ਸ਼੍	
T-1997; V-1997; V-1997;	PR PR XX	1698 GCTATGCTGGCGGGCAGAGCTGGCCCAGGGGAAGTTGCTAAAGGATGTCTTCCGGCCTG 1757
13-MAR-2003. 16-OCT-2001; 2001US-00978564.	PF XX	1638 CATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCAGCAGTCCCCATTCCTGG 1697
Homo sapiens. US2003050241-A1.	P X S X	1578 TTCGCTATGATCTCACCACAGAGAGCCAATTCGGGACCCCCAGGGGCACTGTATGGCCA 1637
	X X X X X X	AGCGGGGCCTGTGGGGTGCTTCCTGGCTTTACAAGCATATCTTCCCCTTCTCCTTGA
Novel human secreted and transmem Human; secreted and transmembrane chromosome identification: vaccin	X X X DE	1458 AGGTGCTGGAGACATATGGACTGACAGAGGGCAACGTGGCCACCATCAACTACACAGGAC 1517
ADA24640; 20-NOV-2003 (first entry)	AX EX	1398 TGGGCAGCGGGCTGCGCCAGATACCTGGGAGCGTTTTGTGCGGGCGCTTCGGGCCCCTGC 1457
ULT 13 .24640 ADA24640 standard; cDNA; 2574 BP.	RES ADA ID XX	1338 GATACCTTGTCAACCAGCCCCGAGCAAGGCAGAACGTGGCCATAAGGTCCGGCTGGCAG 1397
2358 ATTTTGTAATAAATGTGGCTGGAG 	D Q	TCTGGGAAGATTGCCAGCAGCACAGGGTGACGGTGTTCCAGTACATTGGGGAGCTGTGCC
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ne protein; PRO; gene; ss; tissue typing; ine; cancer; retinal disorder; osteoarthritis; rheumatoid arthritis; s; hearing loss; kidney disorder; nervous system disorder; mbrane protein PRO703 cDNA.

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arthritis,
                                                                                                                                            The invention describes an isolated secreted and transmembrane (PRO) polypeptide (I). PRO337 polypeptide is useful for detecting PRO4993 polypeptide in a sample, and vice versa. PRO725, PRO700 and PRO739 are useful for detecting PRO1559 polypeptide in a sample, and PRO1559 is useful for detecting PRO725, PRO700 and PRO739 in a sample. PRO4993 is useful for linking a bioactive molecule to a cell expressing a PRO337 polypeptide, and PRO337 is useful for linking a bioactive molecule to a cell expressing a PRO493 polypeptide. PRO1559 is useful for linking a bioactive molecule to a cell expressing a PRO493 polypeptide. PRO1559 is useful for linking a bioactive molecule to a cell expressing a PRO493 polypeptide. PRO1559 is useful for linking a bioactive molecule to a cell expressing a PRO735, PRO700 and PRO739
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P-PSDB; ADA24641.
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                                                                                                                                                                                                                                                                                                                         isolated PRO polypeptides for example extracellular, secreted and brane bound proteins, useful for modulating the biological activities cells and for treating, for example diabetes, cancer, rheumatoid hritis, and hearing loss.
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                               CGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTTCGGAAGG
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, Godowski PJ, Grimaddi JC, Gurney AL, Hillan KJ;
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Dy 1998 TGGACCTTATGCAGCTCTACACCCACGTCTCTGAGAACTTGCCACCTTATGCCACGTATATGCAGCTCTACACCCACGTCTTCTGAGAACTTGCCACCTTATGCCAGCTCCACGTCTCTACACCCACGTCTTGAGAACTTGCCACCTTATGCCAGCCCCC 2057 2058 GATTCCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCCTTCAAACAGCAGAAAGTTC 2117 2114 GATTCCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCCTTCAAACAGCAGAAAGTTC 2177 2118 GGATGGCAAATGAGGGCTTCGACCCCAGCACCACAGAGACCCACTGTACGTTCTGGACC 2177 2119 GGATGGCAAATGAGGGCTTCGACCCCAGCACCCACTGTACGTTCTGGACC 2177 2178 AGGCTGTAGGTGCCTACACCCCAGCACCTGTCTGACCACTGTACGTTCTGGACC 2233 2178 AGGCTGTAGGTGCCTACCTGCCCCTCACAACTGCCCGGTACAGCACCTCCTGGCAGGAA 2237 2238 AGGCTGTAGGTGCCTACCTGCCCCTCACAACTGCCCGGTACAGCCCTCCTGGCAGGAA 2237 2238 AGGCTGTAGGTGCCTACCTGCCCCTCACAACTGCCCGGTACAGCCCCTCCTGGCAGGAA 2237 2238 ACCTTCGAATCTGAGAACTTCCACACCTGAGAGAGAACTCTGTGGGGTGG 2297 2294 ACCTTCGAATCTGAGAACTTCCACACCTGAGGACCCTGAGAGAACTCTGTGGGGTGG 2297	1814 GGGATGTTTCTTCAACACTGGGGACCTGCTGCTGTCTGCGATGACCAAGGFTTTCTCCGCTGCTGTGTGGACAAGGFTTTCTCCGCTGCTGCTGCGATGACCAAGGFTTTCTCCGCTGCTGCTGCTGCAACCGAGGTTGAAGGGGGAGAATGTGGCCACAACCGAGGTGAACCGAGGTGAACCGAGGTGAACCGAGGTGAACCGAGGTGAACCGAGAACCGAGGTGAACCGAACCGAGGTGAACCGTACCGAGGCCCTAGAACCGAGGTGAAACGAACCGAGGTGAACCGTATCGAAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATGGAGTCACTGTGAAGTCACTGTGAAGGTCTTCGAGGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATGGAGTCACTGTGAATTTCTTCAGGAGGTGAACGTCTATGGAGTCACTGTGAAGGCAGGC	1578 TICGUIATGATGTUACACAGAGAGCUATTUGGGACUCCUAGGGCACTGTATGGCCA 1634 TTCGCTATGATGTUACACACAGAGAGCCAATTUGGGACCCCAGGGGCACTGTATGGCCA 1638 CATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCAGCAGTCCCCATTCCTGG	1398 TGGGCAGCGGCTGCGCCCAGATACCTGGGAGCGTTTTGTGCGGCGCGTTCCGGGCCCTGC 1	Db 1214 AAGATGTGATCTACCTCGCCCTCCCACTCTACCACATGTCCGGTTCCCTGGTCAGTCG 1273 Qy 1218 TGGGCTGCATGGGCATTGGGGCCACAGTGGTGCTGAAATCCAAAGTTCTCGGCTGGTCAGT 1277 Db 1274 TGGGCTGCATGGGCATTGGGGCACAGTGGTGCTGAAATCCAAAGTTCTCCGGCTGGTCAGT 1333 Qy 1278 TCTCGGAACAATTGCCCACACAGGGTGACGTTCCAGTACATTGGGGAGCTGTGCC 1337

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31-MAR-1998; 31-MAR-1998; 01-APR-1998; 01-APR-1998; 01-APR-1998; 08-APR-1998; 08-APR-1998; 08-APR-1998; 09-APR-1998; 09-APR-1998; 09-APR-1998;	PR 20-MAR-1998; 98US-0079895EP. PR 20-MAR-1998; 98US-0078939P. PR 20-MAR-1998; 98US-0078939P. PR 20-MAR-1998; 98US-007995EP. PR 27-MAR-1998; 98US-0079663P. PR 27-MAR-1998; 98US-0079664P. PR 27-MAR-1998; 98US-0079688P. PR 27-MAR-1998; 98US-0079728P. PR 27-MAR-1998; 98US-0079728P. PR 30-MAR-1998; 98US-0079728P. PR 30-MAR-1998; 98US-0079728P. PR 30-MAR-1998; 98US-0079728P. PR 31-MAR-1998; 98US-0079928P. PR 31-MAR-1998; 98US-0079928P. PR 31-MAR-1998; 98US-0079928P. PR 31-MAR-1998; 98US-0080107P.	17-OCT-1997; 03-NOV-1997; 13-NOV-1997; 13-NOV-1997; 10-MAR-1998; 11-MAR-1998; 11-MAR-1998; 11-MAR-1998; 12-MAR-1998; 13-MAR-1998; 20-MAR-1998;	Homo sapiens. US2003050240-) 13-MAR-2003. 16-OCT-2001;	O8-SEP-2003 (first entry) XX XX DE Novel human secreted and transmembrane protein PRO703 cDNA. XX XX Human; secreted and transmembrane protein; PRO; cell death; neuropathy; when the peripheral neuropathy; diabetic peripheral neuropathy; when the peripheral neuropathy; Charcot Marie-Tooth disease; where the peripheral rangier disease; where the peripheral rangier disease; which compare the peripheral rangier disease; where the peripheral rangier disease; where the peripheral rangier disease; we will be provided by the peripheral rangier disease; we be peripheral rangier disease; which compared the peripheral rangier disease; we be peripheral rangier disease; which compared the peripheral rangier disease.	2298 GGGCCGTTGCA
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16-JUN-1999; 99US-01142680P-
26-JUL-1999; 99US-01146282P-
28-JUL-1999; 99US-0146228P-
28-JUL-1999; 99US-0162506P-
30-NOV-1999; 99WO-US028551.
102-DEC-1999; 99WO-US031231.
302-DEC-1999; 99WO-US031274.
05-JAN-2000; 2000WO-US000277.
06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US00376.
11-FEB-2000; 2000WO-US005004.
21-MAR-2000; 2000WO-US005004.
22-MAR-2000; 2000WO-US005019.
21-MAR-2000; 2000WO-US0014941.
102-JUN-2000; 2000WO-US015264.
22-JUN-2000; 2000WO-US032678.
20-JUN-2001; 2001WO-US032678.
20-JUN-2001; 2001WO-US00520.
22-MAR-2001; 2001WO-US00520.
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Ferrara N, 1
Goddard A, (
Kljavin IJ,
Stewart TA,
                                                                                                                                                                                                                                                                     The invention describes an isolated, secreted and transmembrane polypeptide, termed PRO polypeptide (I). (I) is useful for detecting PRO4993, PRO37, PRO1559, PRO7705, PRO700 or PRO739 polypeptide, and for linking a bloactive molecule to a cell expressing the above polypeptides. The bloactive molecule is a toxin, radiolabel or an antibody and causes cell death. (I) is useful as therapeutic agent, in medical and industrial applications e.g. for treating neuropathy, especially peripheral neuropathy, diabetic peripheral neuropathy, AIDS-associated neuropathy, Charcot-Marie-Tooth disease, Refusum's disease, Abetalipoproteinaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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E B, Fong S, Gao W, Gerber H, Gerritsen ME;
PJ, Grimaldi JC, Gurney AL, Hillan KJ;
Napier MA, Pan J, Paoni NF, Roy MA, Shelt,
Williams PM, Wood WL;
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A, Accession: JW0107 A, MOLECULE Type: mRNA A) Residues: 1-669 GBRA A) Cross references: GB.AJ223959 A) Cross references: GB.AJ223959 A) Cross references: GB.AJ223959 A) Experimental source: liver C; Comment: This protein likely functions as a plasma membrane transporter of long chain cids C; Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate-CoA ligase homory F;169-647/Domain: acetate-CoA ligase homology AACL- Ouery Match Best Local Similarity 39.5%; Peed: No. 3, 88-79; Matches 280; Conservative 93; Mismatches 257; Indels 78; Gaps 8; Matches 280; Conservative 93; Mismatches 257; Indels 78; Gaps 8; Matches 280; Conservative 93; Mismatches 257; Indels 78; Gaps 8; Matches 280; Conservative 93; Mismatches 257; Indels 78; Gaps 8; Matches 280; Conservative 93; Mismatches 257; Indels 78; Gaps 8; Matches 280; Conservative 93; Mismatches 257; Indels 78; Gaps 8; Matches 280; Conservative 93; Mismatches 257; Indels 78; Gaps 8; Matches 280; Conservative 93; Mismatches 257; Indels 78; Gaps 8; Matches 280; Conservative 93; Mismatches 257; Indels 78; Gaps 8; Matches 280; Conservative 93; Mismatches 257; Indels 78; Gaps 8; Matches 280; Conservative 93; Mismatches 257; Indels 78; Gaps 8; Matches 280; Conservative 93; Mismatches 257; Indels 78; Gaps 8; Matches 280; Conservative 93; Mismatches 257; Indels 78; Gaps 8; Matches 280; Conservative 93; Mismatches 257; Indels 78; Gaps 8; Matches 280; Conservative 93; Mismatches 257; Indels 78; Gaps 8; Matches 280; Conservative 93; Mismatches 257; Indels 78; Gaps 8; Matches 280; Conservative 93; Mismatches 257; Indels 78; Gaps 8; Matches 280; Conservative 96; Matches 280; Conservative 96; Mismatches 257; Indels 78; Gaps 8; Matches 280; Conservative 96; Mismatches 257; Indels 78; Gaps 8; Matches 280; Conservative 96; Mismatches 257; Indels 78; Gaps 8; Matches 280; Conservative 96; Mismatches 257; Indels 78; Gaps 8; Mismatches 280; Conservative 96; Mismatches 257; Indels 78; Gaps 8; Mismatches 257; Indels 78; Gaps 8; Mismatches 257; Indels 78; Gaps 8; Mismatches 257;	30 276.5 7.2 562 2 AB0253 31 273.5 7.1 561 2 B89943 32 273.5 7.1 562 2 F85791 33 273.5 7.1 524 2 H75530 34 272.5 7.1 503 2 E78053 35 269.5 7.0 561 1 S41589 36 269.5 7.0 999 2 B70501 37 269 7.0 510 2 C97561 38 269 7.0 510 2 C97561 40 268 7.0 512 2 T41161 40 268 7.0 516 2 H83132 41 267.5 7.0 639 2 AB3456 42 267.5 7.0 639 2 AB3456 43 266 6.9 562 2 B83233 44 265.5 6.9 561 2 AC0725 45 264 6.9 562 2 B83233 46 265.5 6.9 561 2 AC0725 47 264 6.9 569 2 D82824 RESULT 1 JW0107 Very-long-chain acyl-CoA synthetase related protein - mouse NyAlternate names: VLACSR C;Species: Mus musculus (house mouse) C;Accession: JW0107; MUID:98308102; PMID:9642112 A,Fafterence number: JW0107; MUID:98308102; PMID:9642112

Minimum DB Maximum DB

Total number of hits satisfying chosen parameters:

Scoring table: Sequence: Title: Perfect score: Run on:

OM protein - protein search, using sw model

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  EPLEDSEGLCIPCOPGEPGLLVGQINQODPLRFDGYV-SDSATNKKIAHSVFRKGDSAY
                                     EPIRDPOGHCMATSPGEPGLLVAPVSQQSP---FLGYAGGPELAQGKLLKDVFRPGDVFF
                                                                              IWEEFTQRFGVPQIGEFYGATECNCSIANMDGKVGSCGFNSRILTHVYFIRLVKVNEDTM
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tive 79; Mismatches 197;
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B87534

R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, J.; Durkin, A.S.; Gwinn, M.L.; Heidelberg, J. Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Heidelberg, J. R.; Itaub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A; Title: Complete Genome Sequence of 4136-4141, 2001

A; Title: Complete Genome Sequence of 4136-4141, 2001

A; Reference number: A87249; MUID:21173698; PMID:11259647

A; A; Ceterica: R87534
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C;Superfamily: Mycobacterium tuberculosis probable fadD6 protein;
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A;Gene: CC2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-635 <STO>
A;Cross-references: GB:AE005673; NID:g13423818; PIDN:AAK24270.1; GSPDB:GN00148
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Best Local 9
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LVLRPPHALDLMQLYTHVSENLPPYARPRFLRLQESLATTETFKQQKVRMANEGFDPSTL
                                                                                                                                                                                                                                           RRFGPLQYLETYGLTEGNVATINYTGQRGAVGRASWLYKHIFPFSLIRYDVTTGEFIRDP
                                                                                                                                                                                                                                                                                                                                                                                                            PKAARISHLKI-LQCQGFYQLCGVHQEDVIYLALPLYHMSGSLLGIVGCMGIGATVVLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WGPDGGDSGEGSAGEGERAAPGAGDAAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTGDLLVCDDQGFLRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQEVNVYGVTVPGHE
                                                                                                                                                                             QGHCMATSPGEPGLLVAPVSQ--QSPFLGYAGGPELAQGKLLKDVFRPGDVFFNTGDLLV
                                                                                                                                                                                                                                                                                                                        KFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPPSKAERGHKVRLAVGSGLRÞDTWERFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                      QLERHMQQWVLGP-VHDDQRDLLKALKSCSQLRPDRETAREGLTASDTALYIYTSGTTGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAGPEFLWLWFGLAKAGLRTAFVPTALRRGPLLHCLRSCGARALVLAPEFLESLEPDLPA
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                                                             VDHDGYIYFIDRIGDTFRWKGENVATSEVAERLAGFEGVLEVNVYGVKVGDLDGKAGMAS
                                                                                          CDDQGFLRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQEVNVYGVTVPGHEGRAGMAA
                                                                                                                                        DGCCIEAGPEEVGECIGHIGSDARSNFTGYA-DKAATEKKVLHDVFEKGDAWFRTGDLMK
                                                                                                                                                                                                                    DRFKVGDVLEFYGATEGNVSFFNFDGKRGAIGRIPSYLRKKFNIRIVKFDVETETPIRGP
                                                                                                                                                                                                                                                                                                 KFSATHFWPEIVAEQCTMFVYIGELCRYLANQPEHELERAHKLRMIFGNGLRADVWDDML
                                                                                                                                                                                                                                                                                                                                                                           PKAARITHMRAQLYMRGPAGSTGAKDTDRIYITLPLYHATGGLCALGAALLNGGSVVLRK
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41.4%; Pre
72;
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Pred. No. 2.4e-63;
'2; Mismatches 239;
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Nature 406, 959-964, 2000
Nature 406, 959-964, 2000
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa A;Reference number; A82950; MUID:20437337; PMID:10984043
A;Accession: H83284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable very-long-chain acyl-CoA synthetase PA2893 [imported] - Pseudomona.
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: H83284
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A; Residues: 1-608 <STO>
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Best Local
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                                                                                            GDLLVCDDQGF--LRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQEVNVYGVTVPGHE
                                                                                                                                                             GEPIRDPQGHCMATSPGEPGLLVAPVSQQSPFLGVAGGPELAQGKLLKDVFRPGDVFFNT
GRCGMAALRLADGVELDRDALAAHLDRELPAYATPVFLRLLREVETTGTFKYKKTDLKRD
                             GRAGMAALVLRPPHALDLMQLYTHVSENLPPYARPRFLRLQESLATTETFKQQKVRMANE
                                                                GDLM--RDIGFKHTQFVDRLGDTFRWKGENVSTTEVENALGAFDGVEDAVVYGVEIPGTN
                                                                                                                               DRPVRDAKGFMEKVGKGEVGLLISEISAKWPFDGYT-DPAKSEAVILRDVFKKGDAWFNT
                                                                                                                                                                                                SIWAEFKORFEIORITEFYASSEGNIGFTNVFNFDNTVGFSPATY
                                                                                                                                                                                                                              DTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASWLYKHIFPFSLIRYDVTT
                                                                                                                                                                                                                                                               AAMALRRKFSASGFWKDVQHYRATCFGYIGELCRYLLNQPPCAEERGNSLTCMIGNGLRP
                                                                                                                                                                                                                                                                                               ATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPPSKAERGHKVRLAVGSGLRP
                                                                                                                                                                                                                                                                                                                              SGTTGLPKASIMSHGKWIKAYGGFGHSGLGLGRDDVLYLTLPCYHNNAVTVCWSAALAGG
                                                                                                                                                                                                                                                                                                                                                            SGTTGLPKAARISHLKILQCQGFY--QLCGVHQEDVIYLALPLYHMSGSLLGIVGCMGIG
                                                                                                                                                                                                                                                                                                                                                                                                 CYWVDDGDTLGDPGSPPMGWRNLMRLAQGQTSENLEDTGRV-----RLKDSCFYIYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80;
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Pred. No. 1e-54
80; Mismatches
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K.R.; Kas,
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Larbig,
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K.; Lim,
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RESULT 6
D70609
D70609
probable fadD6 protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 18-Aug-2000
C;Accession: D70609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: CESP:D1009.1
A;Gene: CESP:D1009.1
A;Introns: 2/2; 60/2; 89/3; 125/3; 192/1; 344/2; 399/1; 547/3;
A;Introns: 2/2; 60/2; 89/3; 125/3; 192/1; 344/2; 399/1; 547/3;
A;Introns: 2/2; 60/2; 89/3; 125/3; 192/1; 344/2; 399/1; 547/3;
A;Introns: 2/2; 60/2; 89/3; 125/3; 192/1; 344/2; 399/1; 547/3;
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submitted to the EMBL Data Library, Novemb
A;Description: The sequence of C. elegans
A;Reference number: Z18422
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T15879
hypothetical protein D1009.1 - Caenorha
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision
C;Accession: T15879
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A; Residues: 1-655 < FAV>
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197; Conserv
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Pred. No. 1.5e-51;
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Nature 393, 537-544, 1998

A;Authors: Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, Taylor, K.; Whitehaad, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: D70609

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-597 COLD
A;Cross-references: GB:Z93777; GB:AL123456; NID:93261726; PIDN:CAB07829.1; PID:91929080
A;Experimental source: strain H37Rv
C;Generics:
A;Gene: fddD6
C;Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate-CoA ligase hom F;93-555/Domain: acetate-CoA ligase homology ACLD
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QAYG-ADIEDPLYVLAGPDEGYVP
                                                                                                                                                            FNTGDLLVCDDQGFLRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQEVNVYGVTVPGH
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                             EGFDPSTLSDPLYVLDQAVGAYLP
                                                            GGRAGMAAITLRAGAEFDGQALARTVYGHLÞGYALÞLFVRVVGSLAHTTTFKSRKVELRN
                                                                                                                             FNTGDVMSPQGMGHAAFVDRLGDTFRWKGENVATTQVEAALASDQTVEECTVYGVQIPRT
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Pred. No. 1.8e-50;
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RESULT T21498

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A;Title: PKC1, encoding a protein kinase C, A;Reference number: Z22303; MUID:98415124; i A;Accession: T43052
A;Status: preliminarr.
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A;Introns: 55/2; 87/2; 120/3; 187/1; 241/1; 356/1; 395/1; 600/1
A;Introns: 55/2; 87/2; 120/3; 187/1; 241/1; 356/1; 395/1; 600/1
C;Superfamily: Mycobacterium tuberculosis probable fadD6 protein;
F;123-609/Domain: acetate-CoA ligase homology <ACL>
                                                                                                                 fatty acid transport protein - fungus (Cochliobolus heterostrophus)
C;Species: Cochliobolus heterostrophus, Bipolaris maydis
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 02-C;Accession: T43052
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A;Molecule type: DNA
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Best Local Similarity
Matches 188; Conserv
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                                                                                                                                                                                                                                                                    590
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                                                                                                                                                                                                                                                                                                                                                                                                                                      LAQGKLLKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGENVATTEVAEVFEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDVVALYMENSVEFVAAMMGLAKIGVVTAWINSNLKREQLVHCITASKTKAIITSVTLQN
                                                                                                                                                                                                                                                                                                                                                                      WLYKHIFPESLIRYDVTTGEPIRDPQGHCMATSPGEPGLLVAPVSQQSPFLGYAG--GPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erghkvrlavgsglredtwerfyrregelqvletygltegnvatinytgqrgavg--ras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTAAGILGVGQALLGGSSCVIRKKFSASNFWRDCVKYDCTVSQYIGEICRYLLAQPVVEE
                                                                                                                                                                                                                                                                                                   LRLQESLATTETFKQQKVRMANEGFDPSTLSDPLYVLDQAVGAYLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPPSKA
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                                                                                                                                                                                                                                                                  MRICQDVEKTGTFKLVKTNLQRLGIMDAP-SDSIYIYNSENRNFVP
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Pred. No. 2.8e-50;
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           from GB/EMBL/DDBJ
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                                                and FAT1, encoding PMID:9742699
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                                                                     fatty
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                                                                     acid transporter
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A;Molecule type: DNA
A;Residues: 1-643 < COS>
A;Cross-references: EMBL
A;Experimental source: s:
C;Genetics:
                                                                                        RESULT 9
$45899
$45899
probable membrane protein YBR041w - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein YBR0411
C/Species: Saccharomyces cerevisiae
C/Jate: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 02-Sep-2000
C/Accession: $45899
C/Accession: $45899
R/Andre, B.; Cziepluch, C.; Hein, C.; Jauniaux, J.C.; Urrestarazu, A.; Viss:
submitted to the Protein Sequence Database, August 1994
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                    A; Molecule type: DNA
A; Residues: 1-623 < AND>
                                                            A;Reference number: S45893
A;Accession: S45899
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mes. 194; Conserv
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                                                                                                                                                                                                                                                                                                                                             S--DPLYVLDQAVGAYLPLTTARYSALLAGNLRI 730
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                                                                                                                                                                                                                                                                                                                                                                                                                      LRPPHALDL--MQLYTHVSENLPPYARPRFLRLQESLATTETFKQQKVRMANEGFDPSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEGRVYFVDRLGDTFRWKSENVSTNEVADVMGTFPQIAETNVYGVLVPGNDGRVRSLNCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DQGFLRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQEVNVYGVTVPGHEGRAGMAALV
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ce: strain C2
    EMBL: Z35910;
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  NID:g536263;
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  PIDN: CAA84983.1;
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PID:g536264;
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      MIPS:YBR041w
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gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; H

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhag.

A;Reference number: A99629; MUID:21156231; PMID:1125;

A;Accession: H90633

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-522 <HAY>

A;Cross-references: GB:BA000007; PIDN:BAB33463.1; PII

A;Experimental source: strain O157:H7, substrain RIMI

C;Genetics:

A;Gene: ECs0040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 2R
(;Superfamily: Mycobacterium tuberculosis probable fadDo
C;Superfamily: Mycobacterium tuberculosis probable fadDo
C;Keywords: transmembrane #status predicted <TM1>
F;1-27/Domain: transmembrane #status predicted <TM2>
F;55-71/Domain: transmembrane #status predicted <TM2>
F;133-623/Domain: transmembrane #status predicted <TM3>
F;149-167/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                   probable crotonobetaine/carnitine-CoA ligase C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul C;Accession: H9063 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurok
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Experimental source: strain C;Genetics:
A;Gene: SGD:FAT1
A;Cross-references: SGD:S00000
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIGYAGGPELAQGKLLKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGENVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATVALLLPAGPEFLWLWFGLAKAGLRTAFVPTALRRGPLLHCLRSCGARALVLAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YGTIIQWFLS--FQQTLVRMDFNDDSVIYRNSKGFCEVAFVGEFGEMLMRIFFFKKFETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KMHKVKVÁYGNGLRÉÐI WODÉRKRÉNI EVI GÉFYAAT ÉAPFATTTF - - ÓKGDEGI GACRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGHKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRAS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPOSITD--TCLYIFTSGTTGLPKAARISHLK-ILQCQGFYQLCGVHQEDVIYLALPLYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIRESEEEIKNALPDVKLNYLE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDYVAIDCTNKPLFVFLWLSLWNIGAIPAFLNYNTKGTPLVHSLKISNITQVFIDPDASN
                                                                                                                                                                                                                                                                                                                                                                                                                                           LNLPSYAMPLEVKEVDEIKMID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -NLPPYARPRFLRLQESLATTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TEVEDQLTASNKEQYAQVLVVGIKVPKYEGRAGFAVIKL-TDNSLDITAKTKLLNDSLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEVAEVFEALDFLQ--EVNVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FOGYLGNAKETKSKVVRDVFRRGDAWYRCGDLLKADEYGLWYFLDRMGDTFRWKSENVST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPLGLTDFKPSMLIYTSGTTGLPKSAIMSWRKSSVGCQVFGHVLHMTNESTVFTAMPLFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---EFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSAEVDGPVPGYLS----
                                                                                                                                                                                                                                 Makino, K.; Ohnishi, M.;
Yasunaga, T.; Kuhara, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                      enome sequence of enterohemorrhagic Escherichia
A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WLYKHIFFFSLIRYDVTTGEFI-RDPQGHCMATSFGEFGLLVA----PVSQQSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGD:S0000245; MIPS:YBR041w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.0%; Score 654; DB 2; 33.7%; Pred. No. 1.8e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84; Mismatches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                             618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    679
                                                                                                                                                                                                                                                                                            18-Jul-2001 #text_change
                                                                                                                                                                                                                                   Kurokawa, I
Shiba, T.;
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                                                                                                                                                                                                                                                                                                                                        [imported] -
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                                                  ; PID:g13359496;
RIMD 0509952
                                                                                                                                                                                                                                                       K.; Ishii,
                                                                                                                                                                                                                                   Hattori,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                          Escherichia coli
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                                                                                                                                                                                                                                   Shinagawa,
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                                                                      GSPDB:GN00154
                                                                                                                                                                                                                                                       Yokoyama,
                                                                                                                                                                                              coli
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                                                                                                                                                                                            genon
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C;Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-522 <STO>
A;Cross-references: GS:AE005174; NID:g12512724; PIDN:AAG54340.1; GSPDB:GN00145; UWGP:Z00
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                              R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
H85484
δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable crotonobetaine/carnitine-CoA ligase caiC [imported] - Escherichia coli (strain C;Species: Escherichia coli (C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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Best Local Similarity
Matches 154; Conserv
                                                                                                                                                              Genetics:
Gene: caiC
                                                Matches 154;
                                                                                                                                        Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: H85484
                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       558 KLLKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGENVATTEVAEVFEALDFL 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 MFYLNISEQEKDTFCERFG-VRLITSYGMTETIVGII---GDRPGDKRRWPSIGRAGFCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 MAAFSAGATFVLVEKYSARAFWGQVQKYRATITECIPMMIRTLMVQPPSANDRQHRLREV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 DGGDSGEGSAGEGERAAPGAGDAAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAG 224
  110 GGCSLAWRLAELAQQRAAHTFLIHGS-----RRFSYSEAERESNRAARAFLRALGWDWGP 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 ALRAMGLHLWAAGPGTHPAGISDLLAEVSAEVDGPVPGY-----LSSPQSITD 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10
                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAEILFTSGTTSRPKGVVITHYN-LRFAGYYSAWQCALRDDDVYLTVMPAFHIDCQCTAA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCLYIFTSGTTGLFKAARISHLKILQCQGFYQL--CGVHQEDVIYLALFLYHMSGSLLGI 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEFLWLWFGLAKAGLRTAFVPTALRRGPLLHCLRSCGARALVLA----PEFLESLEPDLP 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QDIVVVGIK-DSIRDEAIKAFVVLNEGETLSEEEFFRFCEQNMAKFKVPSYLEIRKDL 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QEVNYYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPPYARPRFLRLQESL 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVLE----ADGWLHTGDTGYRDEEGFFYFIDRRCNMIKRGGENVSCVELENIIATHPKI 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KHIFPFSLIRYDVTTGEPIRDPQGHCMATSPGEPG-LLVAPVSQQSPFLGYAGGPELAQG 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQR-----GAVGRASWLY 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQFPSKAERGHKVR-L 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLR----HI-------CLTDVALPADDGVSSFTQLKNQQPATLCYAPPLSTDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEFIFCWFGLAKIGAIMVPINARLLREESAWILQNSQACLLVTSAQFYPMYQQIQQEDAT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGQHLRQMWDDLADVYGHKTALICESSGGVVNRYSYLELNQEINRTANLFY-TLG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.6%; Score 405.5; DB 2; Length 522; 25.8%; Pred. No. 2.2e-20; ative 78; Mismatches 235; Indels 131;
                                                                      10.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----DAEIRD--DHNRPLPAGEIGEICIKGVPGKTIFKEYFLNPK-ATA 396
                                                78;
                                                                      Score 405.5; DB 2;
Pred. No. 2.2e-20;
                                                Mismatches
                                                235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----IRKGDKVALHLDNC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 522;
                                                Indels 131;
                                                                                          Length 522;
                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                D.J.; Mayhev
K.; Apodaca
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Qy Db	10 GGQHLRQMWDDLADVYGHKTALICESSGGVVNRYSYLELNQEINRTANLFY-TLG 63 165 DGGDSGEGSAGEGERAAPGAGDAAAGSGAEFAGGDGAARGGGAAAFLSPGATVALLLPAG 224
Db	64IRKGDKVALHLDNC 77
γ	MLWFGLAKAGLRTAFVPTALRRGPLLHCLRSCGARALVLAPEFLESLEP
g	78 PEFIFCWFGLAKIGAIMVPINARLLREESAWILQNSQACLLVTSAQFYPMYQQIQQEDAT 137
Qγ	-4
م ط	138 QLRHI
Ϋ́	FTSGTTGLPKAARISHLKI
д	180 TABILFTSGTTSRPKGVVITHYN-LRFAGYYSAWQCALRDDDVYLTVMPAFHIDCQCTAA 238
8	387 VGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPPSKAERGHKVR-L 445
дb	239 MAAFSAGATFVLVEKYSARAFWGQVQKYRATITECIPMMIRTLMVQPPSANDRQHRLREV 298
γΩ	FVRRFGPLQVLETYGLTEGNVATINYTGQR
В	299 MFYLNÍSEQEKDTÉCERÉG-VRLÍTSÝGMTÉTTVGTÍGDRÞGDKRRWÞSIGRÁGFCY 354
γŞ	YGWAT
Db	355DABÍRDDHNRPLPAGBÍGEICIKGVPGKTIFKEYFLNÞK-ÁTA 396
Qγ	LKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGENVATTE
Db	ADGWLHTGDTGYRDEEGFFYFIDRRCNMIKRGGENVSCVELENIIATHPK
8	EVNVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPPYARPR
Дb	452 QDIVVVĞIK-DSIRDEAIKAFVVLNEGETLSEEEFFRFCEQNMAKFKVPSYLBIRKDL 508
RESULT 1: S40558 probable C;Species	2 carnitine-CoA ligase (EC 6.2.1) - Escherichia coli (strain K-12 s: Escherichia coli
C; Date:	13-Jan-1995 #sequence_re
R;Blattne	Mau, B.; Shao, Y.
A; Title: The con A; Reference numb	nplete geno oer: A64720
A;Status A;Molecu	LC acid sequence not
A; Cross-	22 <blat> 22 <blat> 23 <b: 1<="" ae000114;="" gb:="" td="" u00096;=""></b:></blat></blat>
A;Expering R;Yura, '	source: strain k-12, substra L, H.; Nagai, H.; Nagata, T. RMRI Data Library. Decembe
A;Descrip A;Referen	Systematic sequencing of the I
A;Access A;Status	2.0
A; Residues:	1-522 < YUR>
A;Cross-refor, 1	erences: EMBL K.; Bourgis, 1
Mol. Microbi	lecular chara
A;Accession	ranslated from GB/EMBL/DDBJ
A; Molecule	type: DNA

K.; Mizobu
of the 0-2

:g1786221;

M.; Co

metabolism

Ni.

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A;Residues: 1-102,'R',104-256,'PR',259-290,'R',292-332,'S',334-349
A;Cross-references: EMBL:X73904; NID:9563860; PIDN:CAA52113.1; PID
A;Experimental source: strain O44 K74
C;Genetics:
A;Gene: caiC
C;Function:
A;Pathway: lysine degradation; tryptophan metabolism
A;Pathway: lysine degradation; tryptophan metabolism
C;Superfamily: 4-coumarate-CoA ligase, acetate-CoA ligase homology
C;Keywords: acid-thiol ligase; ATP; phosphoprotein; transmembrane g;Superfamily: transmembrane #status predicted <TM1>
F;63-521/Domain: transmembrane #status predicted <TM1>
F;81-97/Domain: transmembrane #status predicted <TM2>
F;194/Active site: Lys #status predicted
                                                         RESULT 13
D70806

C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #t
C;Accession: D70806
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.;
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Comnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
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                                                                                                                                                                                                                                                                                                                                    AAHPKIODIVVVGIK-DSIRDEAIKAFVVLNEGETLSEEEFFRFCEONMAKFKVPSYLEI 504
                                                                                                                                                                                                                                                                                                                                                                            EALDFLQEVNVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPPYARPRFLRL
                                                                                                                                                                                                                                                                                                                                                                                                                   PQ-ATAKVLE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RASWLYKHIFFFSLIRYDVTTGEFIRDFQGHCMATSFGEFG-LLVAFVSQQSFFLGYAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLSTDDTAEILFTSGTTSRPKGVVITHYN-LRFAGYYSAWQCALRDDDVYLTVMPAFHID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POSITPTCLYIFTSGTTGLPKAARISHLKILQCQGFYQL--CGVHQEDVIYLALPLYHMS 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEFIFCWFGLAKIG--AIMVPINAR----LICEESAWILONSOACLLVTSAQFYPMYQQI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEFLWLWFGLAKAGLRTAFVPTALRRGPLLHC-----LRSCGARALVLA----
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25.7%; Pre
ative 79;
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A;Gene: fadD17
C;Superfamily: 4-coumarate-CoA ligase; acetat
F;51-486/Domain: acetate-CoA ligase homology
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                            HVSE--NLPPYARPRELRLQESLATTETFKQQKVRMANEGEDPSTLSDPLY
                                                                                        FRWKGENVATTEVAEVFEALDFLQEVNVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYT
                                                                                                                                                                                               TLDTPAGALGP-----LPGGIQIVDPDTGEP----CPTGVVGELVNTAGPG---
                                                                                                                                                                                                                                NYTGORGAVGRASWLYKHIFPFSLIRYDVTTGEPIRDPOGHCMATSPGE-----PGLLV
                                                                                                                                                                                                                                                                                            ELCRYLVNQPPSKAERGHKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVA-TI
FLTEOPDLGHKOWPSYVRVSAGLPRIMTFKVIKROLSAEGV---ACADPVW
                                                               MRVDGENLGTAPIERVLMRYPDATEVAVYPVPDP
                                                                                                                                                             APVSQQSPFLGYAG--GPELAQGKLLKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDT
                                                                                                                                                                                                                                                                KPLSYVLATPELPDDADNPLRAVYGNEGVPGDIDRFGRRFGCV-VMDGFGSTEGGVAITR
                                                                                                                                                                                                                                                                                                                                  DDVCYVSMPLFHSNAVLVGWAVAAACQG---SMALRRKFSASQFLADVRRYGATYANYVG
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                                                                                                                               GFEGYYNDEAAEAE-----RMAGGVYHSGDLAYRDDAGYAYFAGRLGDW
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                                                               ·VVGDQVMAALVLAPGTKFDADKFRA
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enterica

ent

probable crotonobetaine/carnitine-CoA ligase [imported] - Salmonella C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-No C;Accession: AIO510 (;Accession: AIO510 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.;

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;

A;Title: Complete genome sequence of a multiple drug resistant

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AI0510

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-517 <PAR> Skelton, J Salmonella , E.; Wain, J; White, N., enterica Churcher, .; Farrar, ×.

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A;Cross-reference;Genetics:A;Gene:STY0081
C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
G70986
A;Cross references: GB:895890; GB:AL123456; NID:g3242245; A;Experimental source: strain H37Rv C;Genetics: A;Genetics: A;Geneti
                                                                                                                                                                                                                                                                                                                                                   R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Reference number: A70500; MUID:98295987; PMID:9634230
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 18-Aug-2000
C;Accession: G79986
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                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-532 <COL>
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;Genetics:
;Gene: STY0081
                                                                                                                                                                                                                                                                                      Status: preliminary; nucleic
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -DAIRDEAIKAFIVLNEGETLSEAEFFSFCENNMAKFKVPSFMEIRTDL
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   468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
QPDLSTKARPRYIRIAADLPSTATHKVLKRQLIDEGTAVGK-ADTLWVREPRGSAY
                              SENTPPYARPRETRIQESTATTETFKQQKVRMANEGEDPSTLSDPLYVLDQAVGAY
                                                                                           GENVATTEVAEVFEALDFLQEVNVYGVTVPGHEGRAGMAALVLRPPHAL--DLMQLYTHV
                                                                                                                            TTGSGFFTGYYNDPEANAERM-----RHG--MYWSGDLAYRDSEGWIYLAGRTADWMRVD
                                                                                                                                                           VSQQSPFLGYAGGPELAQGKLLKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWK
                                                                                                                                                                                                                        TGQ-----RGAVGRASWLYKHIFFFSLIRYDVTTGEFIRDPQGHCMATSPGEPGLLVAP
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                                                                                                                                                                                                                                                                                                                     TEQDTCYVSMPLFHSNAVVAGWAPAVVSGAAIA-PATFSATGFLDDVRRYHATYMNYVGK
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                                                                GENLTAAPIERILLRYKAINRVAVYAVP-DEYVGDQVMAALVLRAGDTFDPDAFEAFLDA
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                                                                                                                                                                                             PGTPPGSIGRGAHGVAVYNGETVTECAVARFD------AHGALTNADBAIGELVN
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ilarity 27.2%;
Conservative 70
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Pred. No. 1.1e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 532
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Search completed: June Job time : 23 secs 30, 2004, 17:36:06

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
         A Geneseq_29Jan04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2001s:*
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Match
         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              June 30, 2004, 17:23:58; Search time 60 Seconds (without alignments) 3437.661 Million cell updates/sec
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3843
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Copyright (c) 1993 - 2004 Compugen Ltd.
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ABU619
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2759	2759	3474	3525.5	3592	3657	3657	3683	3843	3843	3843	3843	3843	3843	3843	3843	3843	3843	3843	3843
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ALIGNMENTS

AC AAY41699; XX O7-DEC-1999 (first entry) XX Human; PRO703 protein sequence. XX Human; PRO703 protein sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder secreted protein; transmembrane protein. XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; which is a secreted protein; transmembrane protein. XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; which is a secreted protein; transmembrane protein. XX Homo sapiens.	AAY41699 ID AAY	41699 в	tandard; protein; 730 AA.
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31-MAR-1998; 98US-00801 31-MAR-1998; 98US-00801 31-MAR-1998; 98US-00801 01-APR-1998; 98US-00801 01-APR-1998; 98US-00801		31-MAR-1998;	00801
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secreted and transmembrane polypeptides and their polynucleotides ful for treating blood coagulation disorders, cancers and cellular esion disorders.

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Matches 730
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                                                                                                                                        NVATTEVAEVFEALDFLOEVNVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENL
                                                                                                                                                                                        QQSPFLGYAGGPELAQGKLLKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGE
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                                                                  PPYARPRETERLOESLATTETFKOOKVRMANEGFDPSTLSDPLYVLDQAVGAYLPLTTARY
                                                                                                                                                                                                              | QQSPFLGYAGGPELAQGKLLKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGE
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RESULT 2
AAB44255
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AD A425
AD A4255
AD A
Query Match
Best Local Similarity
                                                                                                        AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polyneptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide provide specific targeting of bioactive molecules to cells, AAC78600 to AAC78987 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ashkenazi AJ
Ferrara N,
Goddard A,
Kljavin IJ,
Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-WAR-1999
21-APR-1999
28-APR-1999
11-MAY-1999
23-JUN-1999
26-JUL-1999
29-OCT-1999
02-DEC-1999
02-DEC-1999
02-DEC-1999
                                                                    Sequence
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. Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;

J, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelta

A, Tumas D, Williams PM, Wood WI;
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99US-0123957P.
99US-0126773P.
99US-0130232P.
99US-0131445P.
99US-0141637P.
99US-0145698P.
99US-0145698P.
99WO-US028313.
99WO-US028551.
99WO-US028551.
99WO-US031274.
99WO-US031274.
99WO-US0302777.
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                                                        Human; tumour; diagnosis; neoplastic disease; identification; cartumourigenesis; detection; neoplastic cell growth; proliferation; cytostatic; antiinflammatory; immunomodulatory; inflammatory disc
                                            cytostatic; antiinflammatory; immunological disorder.
                                                                                                          Human
                                                                                                                                 25-JAN-2001
                                                                                                                                                         AAB24054;
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Best Local S
Matches 730
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21-APR-1999;
28-APR-1999;
05-OCT-1999;
30-NOV-1999;
02-DEC-1999;
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N-PSDB; AAC58239.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated antibody for use in compositions and methods for the diagnosis and treatment of neoplastic cell growth and proliferation mammals, including humans, and in monitoring tumor treatment.
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12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                   PLLLLKUHLWPQLRWLPADLAFAVRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAE
                 TAFVPTALRRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAG
                                                                          APGAGDAAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGLAXAGLR
                                                                                                                     LAQQRAAHTFLIHGSRRFSYSEAERESNRAARAFLRALGWDWGPDGGDSGEGSAGEGERA
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99US-0123957P
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99US-0131445P
99WO-US023089
99WO-US028313
99WO-US028551
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RESULT 4
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18-OCT-1999;
25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; fatty acid transporter; PSEC67; long-chain fatty acid uptake; oleic acid; drug screening; gene therapy; metabolic disorder; cardiomyopathy; skeletal muscle disorders; renal failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB60388
                                                                                                                                                                                 WPI; 2001-138349/14.
N-PSDB; AAF27417.
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                                                                                                                                                                                                                                                              Morikawa
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99US-0159586P.
2000UP-00128993.
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Fatty acid transporter protein cDNA library, with activity of molecule of preventives or reme

remedies of fatty-acid metabolic disorders.

Claim 1; Page 48-51;

58pp; Japanese

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AAB83279 standard;
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                                                             06-JUL-2001
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Fatty acid transport protein; FATP; human; mouse; rat; rice blast fungus; yeast; fat absorption; obesity; diabetes; heart disease; hyperlipidaemia; weight control; tuberculosis; TB; anti-fungal.

Homo

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23-SEP-1999; 99US-00405505.
16-DEC-1999; 99US-00465280.
17-FEB-2000; 2000US-00506252.
06-UUL-2000; 2000US-00611197.
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                                                                                        23-SEP-1999;
                                                                                                                                    21-SEP-2000; 2000WO-US025891.
                                                                                                                                                                                29-MAR-2001.
                                                                                          99US-00405504
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(WHED) WHITEHEAD INST BIOMEDICAL (MILL-) MILLENNIUM PHARM INC.

Þ Hirsch DJ, Lodish HF, Gimeno 묪, Tartaglia

2001-354783/37. DB; AAF89054.

New fatty acid transport proteins (FATPs) useful for the manufacture medicament for treating obesity, diabetes and heart disease.

Claim 31; Fig 112; 287pp; English.

The present invention provides the protein and coding sequences of fatty acid transport proteins (FATPs) from a number of species, including FATP1, FATP2, FATP2, FATP4, FATP5 and FATP6 from the human, FATP1-FATP5 from the mouse, FATP3 and b from C. elegans, and FATP from Aspergillus nidulans, Drosophila, zebrafish, Magnaporthe grisea, Mycobacterium tuberculosis and Cochliobolus heterostrophus. The FATP from M. tuberculosis can be used to identify inhibitors which can then be used to treat TB. That from M. grisea (also known as rice blast fungus) can be used to develop anti-fungal agents capable of preventing infection of rice. Those from the human can be used to develop treatments for diabetes, heart disease, obesity, hyperlipidaemia and weight control. The present sequence is one of the sequences described in the exemplification of the invention ght control. The exemplification

Sequence 730 AA;

Query Match

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11-MAR-1998

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12-MAR-1998

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13-MAR-1998
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Ashkenazi AJ, Baker KP, Ferrara N, Filvaroff E, Goddard A, Godowski PJ, Kljavin IJ, Kuo SS, Napi Stewart TA, Tumas D, Wil Napier MA, Pa Williams PM, Botstein D, Desnoyers L, Baton DL; Fong S, Gao W, Gerber H, Gerritsen Grimaldi JC, Gurney AL, Hillan KJ; ier MA, Pan J, Paoni NF, Roy MA, Sh lliams PM, Wood WI; Shelton Ä DL;

WPI; 200 N-PSDB; 2003-328860/31. DB; ACA63545.

New secre secreted as PRO, useful injury, and transmembrane nucleic acids and polypeptides, designated ul for treating inflammation, organ failure, atherosclerosis, ry, infertility, birth defects, premature aging, AIDS, or

12; Fig 39; 453pp; English.

The invention describes an isolated nucleic acid (I) comprising, is at least 80 % sequence identity to, or the full-length coding of, any of 118 300-2100 nucleotide sequences, which encodes its corresponding PRO polypeptide selected from 118 100-700 amino aci sequences, all given in the specification. The nucleic acids and o acid or which

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SALLAGNLRI
                                                             PPYARPRELRLQESLATTETFKQQKVRMANEGFDPSTLSDPLYVLDQAVGAYLPLTTARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISDLIAEVSAEVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQ
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Pred. No. 0;
0; Mismatches
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel method for determining if a nucleic acid coil is a marker for a predetermined phenotype/cell type of interest from a collogical species. The method comprises performing a global comparison of a group of expressed sequence tags (ESTs) known to be expressed in the control of expressed sequence tags (ESTs) known to be expressed in the control of interest with all ESTs expressed in normal tissue control of interest. A method of the invention is useful for collection or cell type of interest from a biological species, preferably control or ruman. The cell type of interest is an abnormal cell such as a tumour cell, and the predetermined phenotype is a stress induced control in also useful for determining the progression of colon cancer in a human, for detecting a tumour cell, and for regulating or cancer in a human, for detecting a tumour cell. An antibody of the invention is cuseful for detecting the absence or presence of peptides encoded by tumour-associated markers. A polypeptide of the invention is useful as an immunogen for vaccinating an animal. The present sequence represents a coll type of the invention of the invention is colon colon control of the invention of the invention is colon colon colon colon control of the invention is colon colo
                                                                                                                                                                                                                      Query Match
Best Local S
Matches 730
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22-OCT-2001; 2001US-0330457P
19-FEB-2002; 2002US-0357144P
                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; marker;
stress-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BIOM-)
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nes 730; Conserv
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                                                                               PILLIKKHKWPQLRWLPADLAFAVRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAE
                                                                                                                                                                    MGVCQRTRAPWKEKSQLERAALGFRKGGSSMFASGWNQTVPIBEAGSMAALLLLPLLLLL
    LAQQRAAHTFLIHGSRRFSYSEAERESNRAARAFLRALGWDWGPDGGDSGEGSAGEGERA
                                                                                                                                    MGVCQRTRAPWKEKSQLERAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLL
                                                  PLLLLKLHLWPQLRWLPADLAFAVRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               if a nucleic acid is a marker for a phenotype/cell type of y global comparison of expressed sequence tags known to be n the phenotype/cell type with all ESTs expressed in normal
                                                                                                                                                                                                                      100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                          AA;
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Pred. No. 0;
O; Mismatches
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RESULT 9
ABU84887
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  17-OCT-1997;
03-NOV-1997;
13-NOV-1997;
21-NOV-1997;
                                                                                                                                                                                                                                                                    Human; thrombolytic agent; interferon; interleukin; cytokine; erythropoietin; colony stimulating factor; cancer; colorectal carcinoma; apoptosis related condition; AIDS; amyotrophic lateral sclerosis; inflammatory disease; asthma; atherosclerosis; neurodegenerative disease; gastrointestinal disorder; Alizhelmer's disease; Parkinson's disease; yastrointestinal disorder; Alizhelmer's disease; parkinson's disease; partension; myocardial ischaemia; kidney disease; carcinogenesis; clomerulonephritis; lung disease; pulmonary hypertension; precelampsia; bronchial asthma; gastric ulcer; renal failure; cardiovascular disease; bronchial asthma; gastric ulcer; renal failure; cardiovascular disease;
                                                                                                                                                                                           US2002177553-A1
                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                         15-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human
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CC The invention relates to an isolated secreted and transmembrane CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful CC in PRO polypeptide detection methods. The PRO polypeptide is useful for CC linking a bioactive molecule to a cell. The PRO polypeptide is useful for CC antibody against it is useful for modulating a biological activity of a CC cell. The PRO polypeptide is useful in industrial applications including pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO polypeptide is useful in industrial applications including CC pharmaceuticals, including set thrombolytic agent, interferon, CC interleukin, erythropoietin, colony stimulating factor and other cytokines. The PRO polypeptide is useful for treating disease such as concer e.g. colorectal carcinoma, apoptosis related conditions e.g. AIDS, CC amportrophic lateral sclerosis; inflammatory disease e.g. Alzheimer's disease, CC amportrophic lateral sclerosis; inflammatory disease e.g. hypertension and CC myocardial ischaemia; kidney disease e.g. hypertension, bronchial CC atthat; gastrointestinal disorders e.g. gastric ulcer and inflammatory CC bowel disease; reproductive disorders e.g. premature labour and CC acid sequence of a PRO polypeptide of the invention. Note: The sequence CC data for this patent did not form part of the printed specification but come obtained in electronic format directly from USPTO at composition of the compart of the printed specification but composition is a proposition of the compart of the printed specification but capture in the composition of the compart of the printed specification but capture in the composition of the compart of the printed specification but capture in the composition of the compart of the printed specification but captured the composition of 
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Stewart TA,
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                                                                                                                                                               PLLLLKLHLWPQLFWLPADLAFAVRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAE 120
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PM, Wood WI;
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21-NOV-1997;
10-MAR-1998;
11-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                 Human, PRO polypeptide; secreted and transmembrane protein; immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia; cardiac insufficiency; nervous system disorder; kidney disorder; bone disorder; cartilage disorder; arthritis; tumour; wound health genetic disorder; cytostatic; antidiabetic; antiinflammatory; antiathritic; anti-tumour; vulnerary; antianaemic; dermatologica.
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17-OCT-1997;
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  81US-00267213.
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Ashkenazi A, Ferrara N, F. Ooo.
Toddard A, Goo.
Twin IJ, Kur
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14-JUN-2001; 2001US-00882336.
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29-JUN-2001; 2001WO-US021066.
09-JUN-2001; 2001WO-US021735.
30-JUL-2001; 2001US-00918585.
Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating cancer, kidney diseases, bone, cartilage disorders and immune deficiencies.
                                                                                           WPI; 2003-288163/28.
N-PSDB; ABX92349.
                                                                                                                                                                                                                                                                                                            GENENTECH INC.
                                                                                                                                                              A, Baker KP, Botstein D, Filvaroff E, Fong S, Ga, Godowski PJ, Grimaldi JC J, Kuo SS, Napier MA, Pan A, Tumas D, Williams PM, 1
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Fong S, Gao W, Gerber H, Gerritsen ME;
Grimaldi JC, Gurney AL, Hillan KJ;
pier MA, Pan J, Paoni NF, Roy MA, Sheltovilliams PM, Wood WI;
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The present invention relates to the isolation of novel human PRO CC polypeptides, and the polynucleotide sequences encoding them. The PRO CC polypeptides are secreted and transmembrane proteins. The PRO CC polypeptides are useful for detecting other PRO polypeptides, for linking CC bioactive molecules to cells expressing PRO polypeptides, for modulating CC biological activities of cells expressing PRO polypeptides, and for for cidentifying agonists or antagonists. The bioactive molecule maybe a CC toxin, radiolabel or antibody, and causes apoptosis or death of the cell. The PRO polypeptides are useful for treating immune disorders, diabetes CC or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system CC disorders, kidney disorders, bone and cartilage disorders or arthritis, tumours, and wound healing. The polypucleotide sequences encoding PRO collegeptides are useful as hybridisation probes, in chromosome and gene CC mapping, in the generation of antisense RNA and DNA, in the preparation CC polypeptides, for generating transgenic animals or knockout CC and in gene therapy. ABUG1071-ABUG1164 represent the human PRO CC polypeptides of the invention. Note: The sequence data for this patent CC sorders users COV/nsipolitic format directly from the USPTO web site at CCC conditions and electronic format directly from the USPTO web site at was obtained in electronic format di seqdata.uspto.gov/psipsDIDEntry.html

AA,

	Query Match	100.0%; Score 3843; DB 6; Length 730;	
	datches 73	Hest Local Similarity 100.03; Fred. No. 0; Matches 730; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Ş	1	MGVCQRTRAPWKEKSQLERAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLLPLLLLL 60	
B	_	MGVCQRTRAPWKEKSQLERAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLL 60	
VQ.	61	PLLLLKLHLWPQLRWLPADLAFAVRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAE 120	
₽. ·	61	PILLIKIHIWPQIRWIPADIAFAVRALCCKRAIRARAIAAAAADPEGPEGGCSIAWRIAE 120	
Ş	121	LAQQRAAHTFLIHGSRRFSYSEAERESNRAARAFLRALGWDWGPDGGDSGEGSAGEGERA 180	
밁	121	LAQQRAAHTELIHGSRRFSYSEAERESNRAARAFLRALGWDWGFDGGDSGEGSAGEGERA 180	
Ś	181	APGAGDAAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGLAKAGLR 240	
D	181	APGAGDAAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGLAKAGLR 240	
Ş	241	TAFVPTALRRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAG 300	
밁	241	TAFVPTALRRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAG 300	
Ś.	301	301 ISDLLAEVSAEVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQ 360	

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RESULT 11
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21-NOV-1997
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97US-0064249P
97US-006631LP
97US-0066364P
98US-0077645P
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98US-007791P
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98US-0079668P
98US-0079766P
98US-0079782P
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98US-00105413
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99US-00311821
99US-00311837
99US-00311837
99US-00311837
99US-00311831
99US-00311837
99U
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480

480 420 420 360

660 660 600 600 540 540

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The invention relates to a new isolated nucleic acid molecule comprises a CC sequence with at least 80% identity to: (a) a nucleotide encoding any of 94 PRO polypeptides whose sequences are fully defined in the CC specification; or (b) any of 94 nucleotide sequences fully defined in the CC specification; or the full length coding sequence of any these 94 cnucleotide sequences. Also included are an isolated PRO polypeptide nucleotide sequences cited above (or an isolated PRO polypeptide polypeptide at least 80% amino acid sequence identity to: (a) an amino acid sequence compared to any of the PRO polypeptide peptide; or (c) an extracellular domain of the PRO polypeptide, or (c) an extracellular domain of the PRO polypeptide, with or CC polypeptide; or (c) an extracellular domain of the PRO polypeptide, with or CC acid molecule, a chimaeric molecule comprising the PRO polypeptide, with or CC polypeptides, a chimaeric molecule comprising the PRO polypeptide, with or CC diagnostics, biosensors or bioreactors. These are particularly useful for cheteting or treating e.g. malignancies or cancers (e.g. ovarian cancer, sarcoma, leukaemia or lymphoma), inflammatory disease, renal disease, arthritis, immune-mediated alopecia, stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The PRO polypeptides are useful in drug screening, particularly as targets of the charaction of the presence of these diseases, and in the diagnostic determination of the presence of these diseases, and in the diagnostic contentification. The PRO genes are useful as hybridisation probes, or for calso be used in gene therapy, particularly for replacing a defective gene. The present sequence represents a PRO polypeptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 730
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Kljavin
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, Godowski PJ, Grimaldi JG, Godowski PJ, Grimaldi JG, Kuo SS, Napier MA, Par MA, Tumas D, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
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Fong S, Gao W, Gerber H, Gerritsen ME;
Grimaldi JC, Gurney AL, Hillan KJ;
Lier MA, Pan J, Paoni NF, Roy MA, Shelt
Lliams PM, Wood WI;
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12-NAR-1998
13-NAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted and transmembrane protein; PRO; tissue typing; chromosome identification; vaccine; cancer; retinal disorder; sports-related joint disorder; osteoarthritis; rheumatoid arthritis; wound healing; obesity; diabetes; hearing loss; cardiac insufficiency disorder; kidney disorder; nervous system disorder; cardiac insufficiency disorder; kidney disorder; nervous system disorder;
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97US-0065364P.

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27-MAR-1999;
28-MAR-1999;
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29-JUN-2000;
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Ferrara N,
Goddard A,
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AJ, Baker K
N, Filvaroff A
A, Godowski P
LJ, Kuo SS,
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  KP, Botstein |
E, Fong S, (
PJ, Grimaldi
Napier MA, P
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    Desnoyers L, Eaton DL;
W, Gerber H, Gerritsen
Gurney AL, Hillan KJ;
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PPYARPRELRIQESIATTETEKQQKVRMANEGEDPSTLSDPLYVLDQAVGAYLPLTTARY
                              PPYARPRELRLQESLATTETEKQQKVRMANEGEDPSTLSDPLYVLDQAVGAYLPLTTARY
                                                                                            NVATTEVAEVFEALDFLQEVNVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENL
                                                                                                                        NVATTEVAEVFEALDFLQEVNVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENL
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Ferrara N,
Goddard A,
Kljavin IJ,
Stewart TA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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IJ, Kuo SS, Nap:
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7, Gurney AL, Hillan KJ;
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                                                                                                                              inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; cancer; diabetic complication; tissue typing; human.
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                                                                                                            Homo sapiens
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2000WO-US0291564.
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PR 20-NOV 1398 98US-0018746.

PR 20-NOV 1398 98US-001864.

PR 20-NOV 1398 98US-002865.

PR 20-NOV 1398 98US-0022654.

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PR 20-NOV 1398 98US-0022654.

PR 20-NOV 1398 98US-0021652.

PR 20-NOV 1398 98US-0021652.

PR 10-NAR 1399 99US-00118256.

PR 110-NAR 1399 99WO-US00522.

PR 111-NAR 1399 99WO-US00522.

PR 112-NAR 1399 99WO-US00522.

PR 114-NAY 1399 99US-0131452.

PR 12-NAR 2000 2000WO-US003555.

PR 11-EBS 2000 2000WO-US003555.

PR 11-EBS 2000 2000WO-US00355.

PR 11-EBS 2000 2000WO-US00355.

PR 12-NAR 2000 2000WO-US00355.
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Search completed: June 30, 2004, 17:30:37
Job time: 65 secs

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Title:
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 SPTREMBL 25:*

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2: sp_bacteria:*
3: sp_fungi:*
4: sp_invertebrat:
6: sp_mammal:*
5: sp_mhc:*
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10: sp_plant:*
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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BC009916; AAH09916.1; AK027499; BAB55156.1;	Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL: BC003441: ABH034411:	Nagahari K., Sugano S., Isogai T.; "HRI human cDNA secquencing project.":	su A., Nagai T., Nakamura Y.,	T., Suzuki Y., Kawai-Hio	UENCE FROM N.A.			"NETO TIMES CONTACTION CONTINUES TO TO TO TO TO THE TOTAL THE TOTA		S., Kimura K., Murakami K., Ishii S., Kawai Y.,	Ishida S., Murakawa K., Ono Y.,	Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara	T., Nagai K., Sugano S.,	., Ota T., Hayashi K.,	F 31-730 FROM N.A.		Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.	Strausberg R.;	TISSUE=Lung;	SEQUENCE FROM N.A.	[1]			tazoa; Chordata;	Homo sapiens (Human).		ဖ	(TrEMBLrel. 25, Last	(TrEMBLrel. 17,	2001 (TrEMBLrel.	; Q96SW5;	Q9BTY5 PRELIMINARY; PRT; 730 AA.	325

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GO; GO:0003824; F:catalytic activity; II
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR000873; AMP-bind.
Pfam; PF00501; AMP-binding; 2.
PROSITE; PS00455; AMP_BINDING; 1.
Hypothetical protein.
SEQUENCE 730 AA; 78644 MW; EBCC4E944
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                                                               EGFDPSTLSDPLYVLDQAVGAYLPLTTARYSALLAGNLRI
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PROSTUE: PSOOLER IN THE BUBL/GenBani DR EMBL; BC029792; AAH29792.1; -...

RGO; GG:003824; F:catalytic activity; IE GG; GG:0008152; P:metabolism; IEA. R InterPro; IFR000873; AMP-bind. R Pfam; PF00501; AMP-binding; 2. Pfam; PF00501; AMP-binding; 2. RROSTUE; PSOOLES; AMP-BINDING; 1. Hypothetical protein.

SEQUENCE 700 AA; 75356 Mu. Amanagement AMP-binding; 2.
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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Hypothetical protein.
Homo sapiens (Human)
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                                                                                                                                                                                           VTTGEPIRDPQGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPELAQGKLLKDVFRPGDVF
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Primates;
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100.0%;
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Pred. No. 1e-244;
0; Mismatches 0
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Best Local S
Matches 526
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-OCT-2003 (TrEMBLrel. 25, Last
Fatty acid transport protein 3 (I
transport protein 3) (Fragment).
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01-NOV-1998
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MEDLINE=983J7965; PubMed=9671728;
Hirsch D., Stahl A., Lodish H.F.;
"A family of fatty acid transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PLASMA MEME
TISSUE SPECIFICITY: LUNG, LIVER, AND TESTIS.

SYNTLARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
COVALENT BINDING OF AMP TO THEIR SUBSTRATE.

L; AF072758; AAC40187.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natl. Acad. Sci. U.S.A. 95:8625-8629(1998).
FUNCTION: INVOLVED IN TRANSLOCATION OF LONG-CHAIN FATTY ACIDS ACROSS THE PLASMA MEMBRANE. MAY PLAY A PIVOTAL ROLE IN REGULA: AVAILABLE LONG-CHAIN FATTY ACID SUBSTRATES FROM EXCGENOUS SOUIN TISSUES UNDERGOING HIGH LEVELS OF BETA-OXIDATION OR
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                             KFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPPSKAERGHKVRLAVGSGLRPDTWERFV
                                                                                                                LPKAARISHLKILQCQGFYQLCGVHQEDVIYLALPLYHMSGSLLGIVGCMGIGATVVLKS
                                                                                                                                                                                  ALRAMGLHLWATGPETNVAGISNLLSBAADQVDEPVPGYLSAPQNIMDTCLYIFTSGTTG
                                                                                                                                                                                                               ALRAMGLHLWAAGPGTHPAGISDLLAEVSAEVDGPVPGYLSSPQSITDTCLYIFTSGTTG
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KFSASQFWDDCQKHRVTVFQYIGELCRYLVNQPPSKAEFDHKVRLAVGSGLRPDTWERFL
                                                                                            LPKAARISHLKVLQCQGFYHLCGVHQEDVIYLALPLYHMSGSLLGIVGCLGIGATVVLKP
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(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
transport protein 3 (FATP3) (Long-chain fatty acid
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83.5%;
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Pred. No. 1.5e-181;
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POTENTIAL.

N-LINKED (GLCNAC. . .) (POTENTIAL)

33C2A558CDD9D989 CRC64;
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PROSITE;
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SLC27A3.
                                                                                                                                                                                                                                                                                                                                    The FANTOM Consortium, the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based 60,770 full-length CDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                        EMBL; AK076014; BAC36120.1; -.
MGD; MGI:J347358; Slc27a1.
GO; GO:0003824; F:catalytic activity;
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR000873; AMP-bind.
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Body;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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TE; PS00455; AMP_BINDING;
NCE 446 AA; 49317 MW;
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                                                             GQFWEDCQQHRVTVFQYIGELCRYLVNQPPSKAERGHKVRLAVGSGLRPDTWERFVRRFG
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            PLQVLETYGLTEGNVATINYTGQRGAVGRASWLYKHIFPFSLIRYDVTTGEPIRDPQGHC
                                                                                                             ARISHLKILQCQGFYQLCGVHQBDVIYLALPLYHMSGSLLGIVGCMGIGATVVLKSKFSA
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                                             SQFWDDCQKHRVTVFQYIGELCRYLVNQPPSKAECDHKVRLAVGSGLRPDTWERFLRRFG
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Rodentia;
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Last annotation updat
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Pred. No. 2.
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BA1ED75849EDF92B CRC64;
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Best Local S
Matches 398
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InterPro; IPR000873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
PROSITE; PS00455; AMP BINDING; 1.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 25, Last samotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to hypothetical protein MGC4365 (Fragment Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrati Mammalia; Eutheria; Primates; Catarrhini; Hominid.
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NON TER 1
SEQUENCE 402 AA; 4
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Submitted
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                                       WKGENVATTEVAEVFEALDFLQEVNVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHV
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91.7%;
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Pred. No. 4.4e-135;
1; Mismatches 0;
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Q8TEJO;
Q8TEJO;
C1-UUN-2002 (TYEMB
01-UUN-2002 (TYEMB
01-CCT-2003 (TYEMB
FLJ00207;
FLJ00207;
Q7726E6 PRELIMINARY; PRT; 619 AA.
Q7726E6 PRELIMINARY; PRT; 619 AA.
Q7726E6 PRELIMINARY; PRT; 619 AA.
Q1726T-2003 (TrEMBLrel. 25, Created)
Q1-QCT-2003 (TrEMBLrel. 25, Last sequence update)
Q1-QCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DKFZp779M0564.
DKFZp779M0564.
Homo sapiens (Human).
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GO; GO:0003824; F:catalyric activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR000873; AMP-bind.
InterPro; IPR000583; GATase 2.
Pfam; PF00501; AMP-binding; 2.
PROSTIE; PS00443; GATASE_TYPE_II; 1.
NON TER
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Eukaryota; Metazoa;
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"The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Spleen;
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hes 269;
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Primates;
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Last annotation update)
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619; 53;

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Q86YF6 PRELIMINARY; PRT; 619 AA.
Q86YF6;
Q1-JUN-2003 (TrEMBLrel. 24, Created)
Q1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Q1-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Similar to VLCS-H1 protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
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Eutheria;
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Primates;
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O9Y2P4;
O9Y2P4;
O1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence
O1-CCT-2003 (TrEMBLrel. 25, Last annotation
Very long-chain acyl-CoA synthetase homolous sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ve
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases EMBL, BC041945; AAH41945.1; -.
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0003152; P:metabolism; IEA.
InterPro; IPR000873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
PROSITE; PS00455; AMP BINDING; 1.
SECUENCE 619 AA; 70101 MW; F995766B7EEB7390 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYARPRELRIQESLATTETEKQQKVRMANEGEDPSTLSDPLYVLDQAVGAYLPLTTARYS
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44.0%; Pred. No. 1.4e
                                                         , Created)
, Last sequence upo
, Last annotation of
ynthetase homolog :
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           Vertebrata;
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P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

A Steinberg S.J., Watkins P.A.;

A Steinberg S.J., Watkins P.A.;

"Human Very Long-Chain Acyl-CoA Synthetase Homolog 1.";

"I "Human Very Long-Chain Acyl-CoA Synthetase Homolog 1.";

RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, AFF04224; AAD29443.1;

DR EMBL, AFF04224; AAD29443.1;

GO; GO:0004467; F:long-chain-fatty-acid-CoA ligase activity; TAS

GO; GO:0004467; F:long-chain-fatty acid metabolism; TAS.

DR GO; GO:000038; P:very-long-chain fatty acid metabolism; TAS.

DR InterPro; IPR000873; AMP-bindd.

DR Pfam; PF00501; AMP-binding; 1.

DR PROSITE; PS00455; AMP_BINDING; 1.

PROSITE; PS00455; AMP_BINDING; 1.
RESULT
Q91WV6
ID QS
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Best Local S
Matches 267
Q91WV6 PRELIMINARY; PRT; 620 AA.
Q91WV6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Solute carrier family 27 (Fatty acid transporter), stC27A2.
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NCBI_TaxID=9606;
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43.8%; Pred. No. 1.9e
tive 103; Mismatches
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Best Local S
Matches 275
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Eukaryota; Metazoa; C.
Mammalia; Eutheria; Ro
NCBI TaxID=10090;
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EMBL; BC022170; AAH22170.1; -.
EMBL; BC024735; AAH24735.1; -.
EMBL; BC024735; AAH24735.1; -.
MGD; MGI:1347099; Slc27a2.
GO; GO:0003824; F:catalytic activity;
GO; GO:0008152; P:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
PR0STITE; P800455; AMP BIXDING;
SEQUENCE 620 AA; 70422 MW;
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275; Conserv
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                                                                                                         DLLVCDDQGFLRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQEVNVYGVTVPGHEGRA
                                                                                                                                                            EPIRDPQGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPELAQGKLLKDVFRPGDVFFNTG
                                                                                                                                                                                         VWRBFIKRFGDIHVYEFYASTEGNIGFVNYPRKIGAVGRANYLQRKVARYELIKYDVEKD
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                  PSTLSDPLYVLDQAVGAYLPLTTARYSALLAGNLRI
                                             GMAALVLRPPHALDLMQLYTHVSENLPPYARPRFLRLQESLATTETFKQQKVRMANEGFD
                                                                                            TWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASWLYKHIFPFSLIRYDVTTG
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PTVIKDTLYFMDDABKTFVPMTENIYNAIIDKTLKL
                                                                                                                                            EPVRDANGYCIKVPKGEVGLLVCKITQLTPFIGYAGGKTQTEKKKLRDVFKKGDIYFNSG
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                                                                                                                                                                                                                                                                                            PKAATINHHRLWYGTGLAMSSGITAQDVIYTTMPLYHSAALMIGLHGCIVVGA
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Rodentia;
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62994BDB1D828B37
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Best Local S
Matches 268
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Submitted (DEC-2002) to the EMBL/GenBan)
EMBL/BC041746, AAH41746.1;
GO; GO:00003824; F:catalytic activity; II
GO; GO:0000152; P:metabolism; IEA.
InterPro; IPRO0873; AMP-bind.
Pfam; PF00501; AMP-binding; 2.
PROSITE; PS00455; AMP_BINDING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8AVC5;
Q8AVC5;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMMBirel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to solute carrier family 27 (Fatty acid transporter),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [SSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
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 652
                                   487
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268; Conserv
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                                                                                                                                     PGLLVAPVSQQSPFLGYAGGPELAQGKLLKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRT
                                                                                                                                                                                  RKYNVTVILYIGEVLRYLCNVPKSDDDVAHNVRMAIGNGLRTDVWSEFLRRFGEIHINEF
                                                                                                                                                                                                                                                                                        QQHRVTVFQYIGELCRYLVNQPPSKAERGHKVRLAVGSGLRPDTWERFVRRFGPLQVLET
                                                                                                                                                                                                                                                                                                                                    LISACGMFEICKVRARDVVYSPLPLYHSSAMMIGVHGCISKGATLVLRPKFSASQFWDDC
                                                                                                                                                                                                                                                                                                                                                       ILQCQGFYQLCGVHQEDVIYLALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGVAKLGCSIACLNNNIRSQSFLHCFRCSRAKVILAEPELKDVIEEVMPELRKDNVKVFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGLAKAGLRTAFVPTALRRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSAGEGERAAPGAGDAAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----MFLEKVERHPDKPFVLFEEEVYTYSHMDKLSNQAARA-LR--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSLAWRLAELAQQRAAHTFLIHGSRRFSYSEAERESNRAARAFLRALGWDWGPDGGDSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPGLLLLPILISFIFPYIFQDIAWFITAVRFGIRI----RRSVSKTPAHTVVD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPLILILELLLIKU--HIWPQURWIPADIAFAVRALCCKRALRARALAAAAADPEGPEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
LYTHVSENLPPYARPRFLRLQESLATTETFKQQKVRMANEGFDPSTLSDPLYVLDQAVGA
                                   GDTFRWKGENVATTEVADILCIVNFIQEVNVYGVSVQNHEGRIGMAALILFDEEVFDGRK
                                                                                                             PGLLICKINSMSPFDGYAGDEHSTERKIMRDVFRKGDAYFNSGDLLTVDQQNFIYFHDRV
                                                                                                                                                                                                                        YGLTEGNVATINYTGQRGAVGRASWLYKHIFPFSLIRYDVTTGEPIRDPQGHCMATSPGE 531
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                                                                                                                                                                                                                                                                                                                                                                                                                            AGPGTHPAGISDLLAEVSAEVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLK
                                                                        GDTFRWKGENVATTEVAEVFEALDFLQEVNVYGVTVPGHEGRAGMAALVLRPPHALDLMQ
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[larity 39.5%;
Conservative 108
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Pred. No. 7.8e-
DB; Mismatches
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Best Local :
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LAMGNGLRADVWETFQQRFGPIRIWEVYGSTEGNMGLVNYVGRCGALGKWSCLLRWLSPF
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Q9Y2P5;
01-NOV-1999
01-NOV-1999
01-OCT-2003
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Genew; HGNC:10999; SLC27A5.
Go; GO:0005783; C:endoplasmic reticulum; TAS.
GO; GO:0004467; F:long-chain-fatty-acid-CoA ligase
GO; GO:00004867; F:long-chain fatty acid metabo
InterPro; IPR000873; AMP-binding; 1.
PROSITE; PS00455; AMP BINDING; 1.
PROSITE; PS00455; AMP BINDING; 1.
SEQUENCE 690 AA; 75384 MW; 011313424D794546 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Very long-chain acyl-CoA synthetase homolog
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Primates; Catarrhini; Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDILINE=99410693; PubMed=10479480;

Steinberg S.J., Wang S.J., McGuinness M.C., Watkins P.A.;

"Human liver-specific very-long-chain acyl-coenzyme A synthetase:
cloning and characterization of a second enzymatically active
protein.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                             GIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPFSKAERGHKVR
                                                                                         TWRSPALFIYTSGTTGLEXEAILTHERVLQMSKMLSLSGATADDVVYTVLPLYHVMGLVV
                                                                                                                                                                                                                                                                                                                                                                                                                RESNRAARAFLRALGWDWGPDGGDSGEGSAGEGERAAPGAGDAAAGSGAEFAGGDGAARG
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                                                                                                                                   SITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYLALPLYHMSGSLL
                                                                                                                                                                                   LVVDPDLRESLEETLPKLQAENTRCFYLSHTSPTPGVGALGAALDAAPSHPVPADLRAGI
                                                                                                                                                                                                                               LVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSAEVDGPVPGYLSSPQ
                                                                                                                                                                                                                                                                        AG----EPTALLVLASQAVPA-LCMWLGLAKLGCPTAWINPHGRGMPLAHSVLSSGARV
                                                                                                                                                                                                                                                                                                                    GGAAAPLSPGATVALLLPAGPEFLWLWFGLAKAGLRTAFVPTALRRGPLLHCLRSCGARA
                                                                                                                                                                                                                                                                                                                                                                    AQPGRA-----LLVWT-GP-----GAGSVTFGELDA-RACQAAWALKAEL--GDPASLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KILHLGLKIR--------
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Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.9%;
42.1%;
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Pred. No. 3.7e-81;
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011313424D794546 CRC64;
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OB 694

OB 694

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OB CC
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PROBLIE; FOUR TRANSPORT;
Glycoprotein; Lipid transport;
SIGNAL 1 26 PC
CHAIN 27 662 PC
TRANSMEM 28 48 P
TRANSMEM 156 176 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BALB/: TISSUE-LIVER;

MEDLINE-98308102; PubMed=9642112;

Berger J., Truppe C., Neumann H., Forss-Petter S.;

Berger J., Truppe C., Neumann H., Forss-Petter S.;

acid transporter protein genes with a distinct expression pattern.

acid transporter protein genes with a distinct expression pattern.

Biochem. Biophys. Res. Commun. 247:2255-260(1998).

-i-FUNCTION: INVOLVED IN TRANSLOCATION OF LONG-CHAIN FATTY ACIDS

ACROSS THE PLASMA MEMBRANE. MAY PLAY A PIVOTAL ROLE IN REGULAT

AVAILABLE LONG-CHAIN FATTY ACID SUBSTRATES FROM EXOGENOUS SOUR

IN TISSUES UNDERGOING HIGH LEVELS OF BETA-OXIDATION OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel. 08, Created)
01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fatty acid transport protein 5 precursor (FATP5) (Lo
acid transport protein 5) (Very-long-chain acyl-CoA
                                                                                                                                         Pfam; PF00501; AMP-binding; 1. PROSITE; PS00455; AMP_BINDING;
                                                                                                                                                                                                                           8888
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MEDLINE=98337965; PubMed=9671728;
Hirsch D., Stahl A., Lodish H.F.;
"A family of fatty acid transporters conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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                                                                                                                                                                                                       GO:0016021; C:integral to membrane; IE; GO:0016021; C:integral to membrane; IE; GO:0003824; F:catalytic activity; IEA. GO:0006865; P:lipid transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PLASMA TISSUB SPECIFICITY: LIVER, BUT NOT IN FETAL LIVER. LOW I BRAIN, LUNG, TESTES, SPLEEN, AND SKELETFAL MUSCLE. SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENT COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRIGLYCERIDE SYNTHESIS.
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AJ223959; CAA11688.1; ALT_INIT.
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Rodentia;
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Transmembrane;
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          (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TREMBLrel. 25, Last annotation update)
1 protein (Solute carrier family 27 (Fatty acid
), member 5).
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M -> MGIWKKLTLLLLLLUGLGQPPWPAAM (;
REF. 2).

K -> I (IN REF. 2).

T -> N (IN REF. 2).

C -> S (IN REF. 2).

N -> K (IN REF. 2).
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Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBanl
EMBL; BC013335; AAH13335.1; -.
EMBL; BC013372; AAH13272.1; -.
PIR; JW0107; JW0107.

GO; GO:0003824; F:catalytic activity; IF
GO; GO:0003824; F:catalytic activity; IF
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR000873; AMP-bind.
Pfam; PF0051; AMP-binding; 1.
PROSITE; PS00455; AMP_BINDING; 1.
Hypothetical protein.
SEQUENCE 689 AA; 76202 MW; 1642BBC20
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TISSUE=Salivary gland;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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80; Conservative
LVKSRLVREGFDVGIIADPLYILDNKAQTFRSLMPDVYQAVCEG
                                                                               YGYTYPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPPYARPRFLRLQESLATTETFK
                                                                                                                            VFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQEVNV
                                                                                                                                                                     PFELVQFDIETAEPLRDKQGFCIPVEPGKPGLLLTKVRKNQPFLGYRGSQAESNRKLVAN
                                                                                                                                                                                      PFSLIRYDVTTGEPIRDPQGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPELAQGKLLKD
                                                                                                                                                                                                                             VRLAMGNGLRANVWKNFQQRFGPIRIWEFYGSTEGNVGLMNYVGHCGAVGRTSCILRMLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDPTCLVLLGLALLGRPWISSWMPHWLSLVGAALTLELLPLQPPPGLRWLHKDVAFTFKM
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                                                                                                             VRRVGDLYFNTGDVLTLDQEGFFYFQDRLGDTFRWKGENVSTGEVECVLSSLDFLEEVNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFYGLKFRRR-----LNKHPPE------TFV-----TFV-----DALERQ 122
                                                       YGVPVPGCEGKVGMAAVKLAPGKTFDGQKLYQHVRSWLPAYATPHFIRIQDSLEITNTYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1251; DB 11;
Pred. No. 1.5e-77;
1; Mismatches 255;
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Best Local
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Q9ES38;
Q9ES38;
01-MAR-2001 (TrEMBLrel. 16
01-MAR-2001 (TrEMBLrel. 20
01-JUN-2003 (TrEMBLrel. 24
Bile acid CoA ligase.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chorda
Mammalia; Eutheria; Rodent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ligase.
SEQUENCE
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Falany C.N., Xie X., Wheeler J., Wang J., Barnes S.;
Falany C.N., Xie X., Wheeler J., Wang J., Barnes S.;
Wholecular cloning and expression of rat liver bile acid
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF242189; AAG09770.1;
GO; GO:0016874; F:11gase activitty; IEA.
GO; GO:0008152; P:metabolism; IEA.
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Pfam; PF00501; AMP-binding; 1.
PROSITE; PS00455; AMP_BINDING;
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                                                                                                                                                      KAERGHKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRAS
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  FLQEVNVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPPYARPRFLRLQESL
                                                                                CFIRMLTPLELVQFDIETAEPVRDKQGFCIPVETGKPGLLLTKIRKNQPFLGYRGSQDET
                                                                                            WLYKHIFPFSLIRYDVTTGEPIRDPQGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPELA
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                          KRKLVANVRQVGDLYYNTGDVLALDQEGFFYFRDRLGDTFRWKGENVSTREVEGVLSILD
                                                                                                                                 PEDKKHTVRFALGNGLRADVWENFQQRFGPIQIWELYGSTEGNVGLMNYVGHCGAVGKTS
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Rodentia;
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Pred. No. 3.
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Sciurognathi; Muridae;
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murinae; Rat
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Db 576 FLEEVNVYGVTVPGCEGKVGMAAVKLAPGKTFDGQKLYQHVRSWLPAYATPHFIRIQDSL 635

Qy 676 ATTETFKQQKVRWANEGFDPSTLSDPLYVLDQAVGAYLPITTARYSALLAGNLRI 730

Db 636 EITNTYKLVKSQLAREGFDVGVIADPLYILDNKAETFRSLMPDVYQAVCEGTWKL 690

Search completed: June 30, 2004, 17:34:58

Job time: 54 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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3843
1 MGVCQRTRAPWKEK
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Match
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          GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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VLCS HUMAN
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VLCS HUMAN
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FAIT PAST
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LCFA ECOSI
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TYCB BREPA
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ENITE ECOLIT
ENITE ECOLIT
TYCC BREDA
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                                  P09095 brevibacill
P3813 b tyrocidin
P39846 bacillus su
P39846 bacillus su
P39846 bacilraci
P17814 oryza sativ
P41636 pinus taeda
P41636 pinus taeda
P39062 bacillus su
P29698 shigella fl
P11454 escherichia
P41656 phycomyces
P23971 bacillus su
P31685 solanum tub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     014975 homo sapien

014975 homo sapien

060714 mus musculu

P97849 rattus norv

P98225 saccharomyc

08xa34 escherichia

P31552 escherichia

08z914 salmonella

08z94 salmonella

08zes9 yersinia pe

08xdr6 escherichia

P29212 escherichia

0838k1 enterococcu

D38135 escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O35488 mus musculu
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45	44	43	42	41	40	39	38	37	36	35	34
214	216	216.5	217.5	217.5	218.5	218.5	218.5	219	219	219.5	219.5
5.6	5.6	5.6	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7
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ACS2_PSEAE	ACSA_RHOCA	LCFA_BACSU	SRF1_BACSU	ACSA_COPCI	ACSA MYCBO	LCFA HAEIN	MENE STAEP	ACSA_DEIRA	4CL1_SOLTU	ACSA_STRCO	ACSA_MYCTU
Q9hv66 pseudomonas	068040 rhodobacter		P27206 bacillus su		P59871 mycobacteri	P46450 haemophilus	Q8cs21 staphylococ	Q9rrl7 deinococcus		Q9x928 streptomyce	069635 mycobacteri

ALIGNMENTS

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RESULT 1
VLCS_MOUSE
VLCS_N
                                Query Match
                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/c; TISSUE=Liver;
MEDLINE=98218572; PubMed=9559670;
Berger J., Truppe C., Neumann H., Forss-Petter S.;
"cDNA cloning and mRNA distribution of a mouse very long-chain acyl-
COA synthetase.";
FEBS Lett. 425:305-309(1998).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Peroxisomal.
-!- TISSUE SPECIFICITY: Strong expression in liver and kidney, low
expression in brain and testis, no expression in skeletal muscle
and spleen.
-!- SUMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
family.
                            TRANSMEM
TRANSMEM
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  035488; 070550;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Very-long-chain acyl-CoA synthetase (BC 6.2.1.-) (Very-long-chain-
                                                                                           EMBL; AF033031; AAB87982.1; -.
EMBL; AJ223958; CAA11687.1; -.
MGD; MGI:1347099; SIC27a2.
InterPro; IFR000873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
PROSITE; PS0045; AMP-BINDING; 1.
Ligase; Fatty acid metabolism; Peroxisome; Transmembrane.
TRANSMEM 1 21 POTENTIAL.
                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=(57BL/6; TISSUE=Liver;
STRAIN=(57BL/6; TISSUE=Liver;
Kemp S., Lu J.-F., Smith K.D.,
Submitted (NOV-1997) to the Ex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fatty-acid-CoA ligase).
SLC27A2 OR FACVL1 OR VLACS OR VLCS.
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70366 MW;
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to the EMBL/GenBank/DDBJ databases
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POTENTIAL.

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Q -> R (IN REF. 2).

Q 77C98BD0DE3B9FFB C
Score 1351;
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DB 1;
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Length 620;
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VLCS RAT

VLCS RAT

VLCS RAT

D VLCS RAT

AC

P97524;

DT

15-JUL-1998 (Rel. 36, Created)

DT

15-JUL-1998 (Rel. 36, Last sequence update)

DT

28-F3B-2003 (Rel. 41, Last annotation update)

DE

Very-long-chain acyl-CoA synthetase (EC 6.2.1.-)

E fatty-acid-CoA ligase,

GN

SLC27A2 OR FACVIOR VLACS.

OS

Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrato;

CM Mammalia; Eutheria; Rodentia; Sciurognathi; Murio

OX

NCBI_TaxID=10116;

RN

(1)

RP

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC

STRAIN=Wistar; TISSUE-Liver;

RA

Hashimoto T.;

"Molecular cloning of cDNA encoding rat very long."
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Sciurognathi; Muridae
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J. Biol. Chem. 271:30360-30
-!- SUBCELLULAR LOCATION: I
-!- SIMILARITY: Belongs to
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| the ATP-dependent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Uchiyama A., Aoyama T., Kamijo K., Wakui K., Fukushima Y., Shimozawa N., Suzuki Y., Kondo N., Orii T., Hashimoto T.; "Molecular cloning of a possible human homolog of the rat very-long-chain acyl-CoA synthetase cDNA and its chromosomal localization."; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria;
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SLC27A2 OR FACVL1 OR VLACS
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:00040873; AMP-bind.
:00040873; AMP-bind
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Catarrhini; Hominidae;
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28-FEB-2003 (Rel. 41, Last annotation update)
Long-chain fatty acid transport protein precu
                                                                                                                                                                                                                                       MEDLINE=95042740; PubMed=7954810;
Schaffer J.E., Lodish H.F.;
"Expression cloning and characterization
chain fatty acid transport protein.";
Cell 79:427-436(1994).
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                its insulin response sequence.";
J. Biol. Chem. 273:27420-27429(1998)
                                                                                                MEDLINE=98438516; PubMed=9765271;
Hui T.Y., Frohnert B.I., Smith A.J.,
"Characterization of the murine fatt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression in spleen or SIMILARITY: Belongs to t
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                                                                                                                                                                                                                                                                           EPIRDPQGHCMATSPGEPGLLVAPVSQQSP---FLGYAGGPELAQGKLLKDVFRPGDVFF
                                                                                                                                                                                                                                                                                                                                                                   IWEEFTQRFGVPQIGEFYGATECNCSIANMDGKVGSCGFNSRILTHVYPIRLVKVNEDTM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVVLRKKFSASRFWDDCVKYNCTVVQYIGEICRYLLRQPVRDVEQRHRVRLAVGNGLRPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPPSKAERGHKVRLAVGSGLRPD 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGTTGLPKAAIVVHSRYYRIAAFGHHSYSMRAADVLYDCLPLYHSAGNIMGVGQCVIYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGTTGLPKAARISHLKILQCQGF-YQLCGVHQEDVIYLALPLYHMSGSLLGIVGCMGIGA
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LONG-CHAIN FATTY ACID TRANSPORT PROTEIN.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

1010892BA8D985B4C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-dependent AMP-binding enzyme
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4.1e-63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seque
28-FEB-2003 (Rel. 41, Last annot
Long-chain fatty acid transport
SLC27A1 OR FATP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FATP_RAT P97849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=98041635; PubMed=9375787;

Schaap F.G., Hamers L., van der Vusse G.J., Glatz J.F.

Schaap F.G., Hamers L., van der Vusse G.J., Glatz J.F.

"Molecular cloning of fatty acid-transport protein cDN

Biochim. Biophys. Acta 1354:29-34(1997).

-i- FUNCTION: Involved in translocation of long-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Lipid
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00501; AMP-binding; 1.
PROSITE; PS00455; AMP_BINDING; 1.
Glycoprotein; Lipid transport; Signal.
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U89529; AAC53424.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interPro;
                                                                                                                                                                                                                                                                Local Similarity
nes 238; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          across the plasma membrane. May play a pivotal role in regu
available long-chain fatty acid substrates from exogenous su
in tissues undergoing high levels of beta-oxidation or
triglyceride synthesis.
SUBCELLULAR LOCATION: Plasma membrane.
SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family.
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SGTTGLPKAARISHLKILQCQGF-YQLCGVHQEDVIYLALPLYHMSGSLLGIVGCMGIGA
                                                                      EPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSAEVDGPVPGYLSSPQSITDTCLYIFT
                                                                                                             VAALLNVNIRREPIAFCIGTSAAKALIYGGEMAAAVAEVSEQIGKSLIKFCSGDIGPESV
                                                                                                                                                 RTAFVPTALRRGPLLHCLRSCGARALVLAPEFL--------
                                                                                                                                                                                     DASSGICWTFAQLDTYS---NAVANLFLQLGFAPGDVVAVFLEGRPEFVGLWLGLAKAGV
                                                                                                                                                                                                                          DAAAGSGAEFAGGDGAARGGGAAAPL-----SPGATVALLLPAGPEFLWLWFGLAKAGL
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Last annotation up
transport protein
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                                                                                                                                                                                                                                                              Score 1052.5;
Pred. No. 7.6e.
78; Mismatches
                                                                                                                                                                                                                                                                                                                                                       LONG-CHAIN FATTY ACID
N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
LONG-CHAIN
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(See http://www.isb-sib.ch/announce/
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7.6e-63;
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                                                                                                                                                                                                                                                                                                                                             CRC64;
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01-OCT-1994
01-OCT-2001
16-OCT-2001
Probable lon
PATI OR YERO
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              entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Disruption of the Saccharomyces cerevisiae homologue to fatty acid transport protein impairs uptake and growth on fatty acids.";
                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-serviced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97236810; PubMed=9079682;
Faergeman N.J., Dirusso C.C., Elberger A., F
"Disruption of the Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              FUNCTION: May be involved in long-chain fatty acids uptake, and thus may play a pivotal role in regulating their accessibility prior to metabolic utilization. May play an important role in uptake of these hydrophobic compounds under conditions where facid synthesis is compromised.

SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCT-1994 (Rel. 30, Created)
CCT-1994 (Rel. 30, Last sequence update)
CCT-2001 (Rel. 40, Last annotation update)
able long-chain fatty acid transport protein.
OR YBR041W OR YBR0411.
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PIR; S45899; S45899.
GermOnline; 138584; -
SGD; S0000245; FAT1.
GO; GO:0005792; C:microsome
GO; GO:0005777; C:peroxisom
GO; GO:0005777; C:peroxisom
GO; GO:0005886; C:plasma me
GO; GO:0005886; P:long-chai
GO; GO:0004467; F:long-chai
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Lipid transport; Transmembrane.
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G0:0005811; C:lipid particle; IDA.
G0:0005792; C:microsome; IDA.
G0:0005777; C:peroxisome; IDA.
G0:0005777; C:peroxisome; IDA.
G0:000586; F:long-chain fatty-acid transporter activity;
G0:000586; F:lipid transport; IMP.
G0:0006869; F:lipid transport; IMP.
G0:0006869; P:lipid transport; IMP.
G0:0000886; P:very-long-chain fatty acid metabolism; IMP.
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TE; PS00455; AMP_BINDING; 1.
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                                                                                                  LNLPSYAMPLFVKFVDEIKMID
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                                                                                                                     -NLPPYARPRFLRLQESLATTE
                                                                                                                                                 TEVEDQLTASNKEQYAQVLVVGIKVPKYEGRAGFAVIKL-TDNSLDITAKTKLLNDSLSR
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Pred. No. 2.9e-36;
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Best Local S
Matches 154
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MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T Iida T., Takami H., Honda T., Sassakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli "Complete genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22 (2001).

-1- FUNCTION: Could catalyze the transfer of CoA to crotonobetai
                                                                                                                                                                                                                                                                                           InterPro; IPR000873; AMP-bind. Pfam; PF00501; AMP-binding; 1. PROSITE; P800455; AMP_BINDING; Ligase; Complete proteome. SEQUENCE 522 AA; 59144 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE-21074935; PubMed=11206551; PubMed=11206551; Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Perna N.T., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB005180; AAG54340.1;
EMBL; AP002550; BAB33463.1;
PIR; H85484; H85484.
PIR; H90633; H90633.
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Probable crotonobetaine/carnitine-CoA
CAIC OR Z0043 OR ECS0040.
Escherichia coli O157:H7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATHWAY: Carnitine metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gamma-butyrobetaine).
SIMILARITY: Belongs to the ATP-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family.
                                                                                                                                                                                                                                 154;
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                                                                                                                                       165
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                                                                                                                                                                                                                                                Similarity
ALRAMGLHLWAAGPGTHPAGISDLLAEVSAEVDGPVPGY
                                              PEFIFCWFGLAKIGAIMVPINARLLREESAWILQNSQACLLVTSAQFYPMYQQIQQEDAT
                                                                          PEFLWLWFGLAKAGLRTAFVPTALRRGPLLHCLRSCGARALVLA---
                                                                                                                                        DGGDSGEGSAGEGERAAPGAGDAAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAG
                                                                                                                                                                      GGQHLRQMWDDLADVYGHKTALICESSGGVVNRYSYLELNQEINRTANLFY-TLG-----
                                                                                                                                                                                                  GGCSLAWRLAELAQQRAAHTFLIHGS-----RRFSYSBAERESNRAARAFLRALGWDWGP
                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                  10.6%;
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                                                                                                                                                                                                                                                  Score 405.5;
Pred. No. 8.
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ligase (EC
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                                                                                                                                                                                                                                                                                              CRC64;
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Tobe T.,
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              LSSPQSITD
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01-JUL-1993
28-FEB-2003
                                                                                               MEDIINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose E
                                                                                                                                                                                                                            MEDLINE=92334977; PubMed=1630901;
Yura T., Mori H., Nagai H., Nagata
Isono K., Mizobuchi K., Nakata A.;
                                                                                                                                                                                                                                                                                                                                          Eichler K., Bourgis F., Mandrand-Berthelot M.-A.
                                                             "The complete genome sequence Science 277:1453-1474(1997).
                                                                                                                                                                                      "Systematic sequencing of the Escherichia
the 0-2.4 min region.";
Nucleic Acids Res. 20:3305-3308(1992).
                                                                                                                                                                                                                           Yura T., Mori H., Isono K., Mizobuc
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=K12;
                                                                                                                                                                                                                                                                                                      Mol.
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metabolism
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.,
STRAIN=044:K74;
                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
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                                                                                                                                                     STRAIN=K12
                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95115548; PubMed=7815937;
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=562;
                       or carnitine.
-!- PATHWAY: Carnitine metabolism
                                                                                       Mau B.,
 gamma-butyrobetaine)
SIMILARITY: Belongs
                                                  FUNCTION: Could
                                                                                                                                                                                                                                                                                                      polism in Escherichia coli."
Microbiol. 13:775-786(1994)
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                                                                                       Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               003 (Rel. 41, Last annotation update) crotonobetaine/carnitine-CoA ligase
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                                                                                                                                                                                                                                                                                                                   characterization of the in Escherichia coli.";
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(Rel. 26, Last sequence up)
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Belongs
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ECOGENE; EG11558; CaiC.
InterPro; IPR000873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
PROSITE; PS00455; AMP_BINDING;
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EMBL; D10483; BAB96606.1; -.
EMBL; AE000114; AAC73148.1;
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                                             PELAQGXLLKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGENVATTEVAEVF
                                                                                        RVGFCYE---
                                                                                                                              RASWLYKHIFPFSLIRYDVTTGEPIRDPQGHCMATSPGEPG-LLVAPVSQQSPFLGYAGG
                                                                                                                                                                            HRLREVMFYLNLSEQEKDAFCERFG-VRLLTSYGMTETIVGII---
                                                                                                                                                                                                                HKVR-LAVGSGLREDTWERFVRRFGELQVLETYGLTEGNVATINYTGQR-----GAVG
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Best Local Similarity
Matches 144; Conser
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STRAIN=Ty2 / ATCC 700931;
STRAIN=Ty2 / ATCC 700931;
STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S. -R., Plunkett G. III
Burland V., Kodoyianni V., Schwartz
Burland V., Kodoyianni V., Schwartz
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";

Nature 413:848-852(2001).
                                                                                                                                                EMBL; AL627265; CAD01225.1; -.
EMBL; AE016834; AA667805.1; -.
EMBL; AE016834; AA67805.1; -.
InterPro; IPR000873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
PROSITE; PS00455; AMP_BINDING;
                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produce between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as impositive and this statement is not removed. Use entities requires a license agreement (See http or send an email to license@isb-sib.ch).
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable crotonobetaine/carnitine-CoA ligase
CAIC OR STY0081 OR T0072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or carnitine (By similarity).
-!- PATHWAY: Carnitine metabolism (conversion
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                                                                                                                                                                                                                                                                                                                                                                      STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Probable crottonobetaine/carnitine-CoA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8ZRX4;
28-FEB-2003
                                                                                                                                                         Nature 413:852-856(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAIC OR STM007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAIC SALTY
                                                                                                                                                                                                             "Complete genome sequence
                           gamma-butyrobetaine)
SIMILARITY: Belongs
                                                                                or carnitine (By similarity).

PATHWAY: Carnitine metabolism (conversion
                                                                                                                                FUNCTION: Could catalyze the transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -EGWLHTGDSGYQDEDGYFYFVDRRCNMIKRGGENVSCVELENIISAHPKIQDIVVVGIK
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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PROSITE; P800455; AMP_BINDING;
Ligate; Complete proteome.
SEQUENCE 517 AA; 58487 MW;
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                                                                                                                                                                                                      TWERFVRREGELQVLETYGLTEGNVATINYTGQR-----GAVGRASWLYKHIPPFSLI
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-DAIRDEAIKAFIVLNEGETLSEAEFFSFCENNMAKFKVPSFMEIRTDL
                            VPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPPYARPRFLRLQESL
                                                                                                                                                                          EKDDFTERFG-VRLLTSYGMTETIVGII---GDRPGDKRRWPSIGRVGFSYE-----
                                                                                                                                                                                                                                    FVLLEKYSARAFWDQVRKYQATVTEC1PMMIRTLMVQPAAPTDRQHHLREVMFYLNLSEQ
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                                                        -EGWLHTGDSGYQDEDGYFYFVDRRCNMIKRGGENVSCVELENIISAHPKIQDIVVVGIK
                                                                                                                                             RYDVTTGEPIRDPQGHCMATSPGEPG-LLVAPVSQQSPFLGYAGGPELAQGKLLKDVFRP
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                                                                                                                 ----ABIRODONRPLPA--GBIGBICIKGIPGKTIFKBYYMOPB-ATAKALBP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 352.5; DB
Pred. No. 3e-16;
4; Mismatches 2
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RESULT 11
LCFA YERPE STANDARD; PRT; 562 AA.
LCFA YERPE STANDARD; PRT; 562 AA.

ID LCFA YERPE STANDARD; PRT; 562 AA.

AC Q8ZES9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-CCT-2003 (Rel. 42, Last annotation update)
DT LOTG-chain-fatty-acid--CoA ligase (EC 6.2.1.3) (Long-chain acyl-CoA proposed or ypo2074 OR Y2236.

GN FADD OR YPO2074 OR Y2236.
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Best Local S
Matches 131
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MEDIINE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.
Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Bl.
Perry R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                            Complete
NP BIND
VARIANT
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PROSITE;
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J. Bacteriol. 184:4601-4611(2002).

-I-FUNCTION: Esterification, concomitant with transport, of exogenous long-chain fatty acids into metabolically active CoA thioesters subsequent degradation or incorporation into phospholipids (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Genome sequence of Yersinia pestis, the causative agent of plague."
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ414151; CAC90886.1; --
EMBL; AE013826; AAM85796.1; ALT_INIT.
PIR; AE0253; AB0253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not remove entities requires a license agreement (so or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00455; AMP_BINDING; 1.
Ligase; Fatty acid metabolism; Magnesium;
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MEDLINE=21470413; PubMed=11586360;
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ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COFACTOR: Magnesium (By similarity).
SUBUNIT: Homodimer (Probable).
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PF00501; AMP-binding; 1
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9; Mismatches
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Pred. No. 3.
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X MEDLINE=21156231; PubMed=11258796;

A Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yoko A Hayashi T., Makino K., Ohnishi M., Murata T., Tanaka M., Tobe A Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Yasun A Kuhara S., Shiba T., Hattori M., Sasakawa C., Ogasawara N., Yasun A Kuhara S., Shiba T., Hattori M., Shinagawa H.;

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DNA Res. 8:11-22(2001).

C long-chain fatty acids into metabolically active CoA thioe for subsequent degradation or incorporation into phospholia
                                                                                                                                                                                                                                                                                                                      Perna N.T., Flunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck B.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K. Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; Groome sequence of enterohaemorrhagic Escherichia coli O157:H7 Nature 409:529-533 (2001).
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Long-chain-fatty-acid--CoA ligase (EC 6.2.1
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MEDLINE=21074935; PubMed=11206551;
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Escherichia coli O157:H7.
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COFACTOR: Magnesium (By similarity)
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                    LOTA ECOLI STANDARD; PRT; 5
P29212;
01-DEC-1992 (Rel. 24, Created)
01-FEB-1994 (Rel. 28, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Long-chain-fatty-acid--CoA ligase (EC
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InterPro; IPR000873; AMP-bind.
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MEDITNE-97251358; PubMed=9097040;
Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Kakino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura Makino K., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; "A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map. DNA Res. 3:379-392(1996).
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                                                                                                                                                                                                                                                     STRAIN=06.HI / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
Melch R.A., Burland V., Plunkett G. III, Redford P., Rc Melch R.A., Burland V., Plunkett G. III, Redford P., Rc Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N Mobley H.L.T., Donnenberg M.S., Blattner F.R.; Mobley H.L.T., Donnenberg M.S., Blattner F.R.; Protessive mosaic structure revealed by the complete ge of uropathogenic Escherichia coli.";

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                                                                                                        IDENTIFICATION OF ATP-BINDING MOTIF, AND MUTAGENESIS OF TYR-21 THR-214; GLY-216; THR-217; GLY-219; LYS-222 AND GLU-361.

MEDLINE=22162442; PubMed=12034706;

Weimar J.D., DiRusso C.C., Delio R., Black P.N.;

"Functional role of fatty acyl-coenzyme A synthetase in the "Functional role of fatty acyl-coenzyme A synthetase in the transmembrane movement and activation of exogenous long-chain acids. Amino acid residues within the ATP/AMP signature motif Escherichia coli FadD are required for enzyme activity and fat
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Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose I
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            for subsequent degradation or incorporation CATALYTIC ACTIVITY: ATP + a long-chain carbo
                                          FUNCTION: Esterification, concomitant with long-chain fatty acids into metabolically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
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EMBL; AE016761; AAN80668.1; ALT_INIT.
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SUBUNIT: Homodimer (Probable).
SUBCELLULAR LOCATION: Partially membrane-associated (Potential).
SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family.
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                                                 ATINYTGQRGAVGRASWLYKHIFPFSLIRYDVTTGEPIRDPQGHCM----ATSPGEPGL
                                                                                                         NTLFNALLNNKEFQQLDFSSLHLSAGGGMPVQQVVAERWVKLTGQ-YLLEGYGLTECAPL
                                                                                                                                                                                                                        HPGKELVVTALPLYHIFALTINCLLFIELGGQNLLITNPRDIPGLVKELAKYPFTAITGV
                                                                                                                                                                                                                                                                                VHQEDVIYLALPLYHMSGSLLGIVGCMGIGA-TVVLKSKFSAGQFWEDCQQHRVTVFQYI
                                                                                                                                                                                                                                                                                                                                                                                SAEVDGPVPGYLSSPQSITDTCLYI-FTSGTTGLPKAARISHLKIL----QCQGFYQLCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLESLEP--DLPA----LRAMGLHLWAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSPGATVALLLPAGPEFLWLWFGLAKAGLRTAFVPTALRRGPLLHCLRSCGARALVLAPE
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Fatty acid met
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NASA
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                                                                                                                                                                                                                                                                                                                                           SALHNGYRMQYV-KPELVPEDLAFLQYTGGTTGVAKGAMLTHRNMLANLEQVNATYGPLL
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0501; AMP-binding; 1.
PS00455; AMP_BINDING;
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T->A: DECREASE IN ACTIVITY.
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E->A: DECREASE IN ACTIVITY.
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Pred. No. 1.2e-10;
7; Mismatches 235;
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GKVDNKA -> QSGQ (IN REF.
; 249B0AA54B3DBFA5 CRC64.
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: 10% OF WILD-TYPE &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;

SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;

MEDLINE=22531367; PubMed=12644504;

Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

Deng W., Liou S.-R., Plunkett D.C., Blattner F.R.;

Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;

Burland v., Kodoyianni v., Schwartz D.C., Blattner Typhi st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Cronin A., Davis P., Davies R.M., Holroyd S., Jagels K., Feltwell T., Hamilin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-S. Typhimmrium; STRAIN=LT2 / SGSC1412 / ATCC 700720; SPECIES-S. Typhimmrium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MCDLINE=21534948; PubMed=11677609; McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latre: McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latre: Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Le Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvand Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
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SPECIES=S.typhi; STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                  J. Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of a multiple enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston R., Wilson R.K.;
"Complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella typhimurium,
Salmonella typhi
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28-FEB-2003 (Rel. 41, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Long-chain fatty-acid--CoA ligase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 413:852-856(2001).
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      + diphosphate + an acyl-CoA,
COFACTOR: Magnesium (By similarity)
SUBUNIT: Homodimer (Probable).
SUBCELLULAR LOCATION: Partially mem
                                                                                                                         similarity).
CATALYTIC ACTIVITY: ATP +
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ou S., Layman |
Mulvaney E.,
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         (Potential)
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RESULT 15
MENE ENTEA

AC Q838K1;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE O-succinylbenzoate--CoA ligase (EC 6.2.1.26)
DE succinylbenzoyl-CoA synthetase).
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Best Local S
Matches 124
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EMBL; AL627272; CAD05501.1; -.
EMBL; AE016837; AA068725.1; -.
StyGene; SG?????; fadD.
InterPro; IPR000873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
PROSITE; P800455; AMP BINDING; 1.
Ligase; Fatty acid metabolism; Magnesium; ATP-binding; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
NP_BIND 213
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                                                                                                                                                           VSENLPPYARPRFLRLQESLATTETFKQQKVRMANE
                                                                                                                                                                                  LVSGFNVYPNEIEDVVMQHSGVQEVAAVGVP-SGSSGEAVKLFVVKKDP-ALTDDALITF
                                                                                                                                                                                                          RWKGENVATTEVAEVFEALDFLQEVNVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTH
                                                                                                                                                                                                                                                        VAPVSQQSPFLGYAGGPELAQGKLLKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTF
                                                                                                                                                                                                                                                                                                        TINYTGQRGAVGRASWLYKHIFFFSLIRYDVTTGEPIRDPQGHCM-----ATSPGEPGLL
                                                                                                                                                                                                                                                                                                                                TLFNALLNNKEFQQLDFSSLHLSAGGGMPVQNVVAERWVKLTGQ-YLLEGYGLTECAPLV
                                                                                                                                                                                                                                                                                                                                                      ELCRYLVNQPPSKAERGHKVRLAVGSGL--RPDTWERFVRRFGPLQVLETYGLTE-GNVA 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAEVDGPVPGYLSSPQSITPTCLYIFTSGTTGLPKAARISHLKIL----QCQGFYQLCGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAHTLEKVVEKTSVQHVILTRMGDQLSTAKGTVVNFVVKYIKRLVPKYH---LPDAISFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSPGATVALLLPAGPEFLWLWFGLAKAGLRTAFVPTALRRGPLLHCLRSCGARALVLAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          561 AA;
                                                                                                                                                                                                                                   - VKGPQVMĹĠŶWQRPD-ATDEIIK---
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ilarity 24.0%;
Conservative 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 265.5; 1
Pred. No. 2.1e.
30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP
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               (OSB-CoA synthetase)
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Query Match
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Matches 119
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Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
"Role of mobile DNA in the evolution of vancomycin-resistant
Enterococcus faecalis.";
Science 299:2071-2074(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PROVIDED: 1.
TIGREAMS; TIGRE1923; menE; 1.
PROSITE; BS00455; AMP BINDING; 1.
Menaquinone biosynthesis; Ligase;
Menaquinone 485 AA; 54289 MW; 1B:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produce between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as imodified and this statement is not removed. Use entitles requires a license agreement (See http or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; EF0446; -. HAMAP; MF_00731; -; 1. InterPro; IPR000873; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22550857; PubMed=12663927;
Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MENE OR EF0446.
Enterococcus faecalis
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=V583 / ATCC 700802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00501; AMP-binding; PRINTS; PR00154; AMPBINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diphosphate + O-succinylbenzcyl-CoA.
PATHWAY: Menaquinone biosynthesis.
SIMILARITY: Belongs to the ATP-dependent
family. MenE subfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COA (OSB-COA).
CATALYTIC ACTIVITY: ATP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Converts O-succinylbenzoate
                                                                                                                                                                                                                                                                                                                                                                                                                                                         217
308
                                       501
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119; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       VALLLPAGPEFLWLWFGLAKAGIRTAFVPTALRRGPLLHCLRSCGARALVLAPEFLESLE
                                                                                                                                                                                                    VGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPPSKAERGH----K
                                                                                                                                                                                                                                                                                                                                                                            PDLPALRAMGLHLWAAGPGTHPAGISDLLAEVS-AEVDGPVPGYLS
                                                                                 GMLLGGGPIAPDKLAQCEEKGIP--VIQSYGMTETCSQVVALKFEDAALKIGSA-----
                                                                                                                     VRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTE--GNVATINYTGQRGAVGRASWLYKH
                                                                                                                                                               VRQLVLGCSIRLYDKFDEQQVTQDLQEGRGTVISVVATMLQQLLSVYP--
                                                                                                                                                                                                                                                VASIMYTSGTTGQPKGV-LQRFKNHLASARGTQENMGITAEDCWLCAVPLFHISG-LSIV
                                                                                                                                                                                                                                                                                    TCLYIFTSGTTGLFKAARISHLK---ILQCQGFYQLCGVHQEDVIYLALPLYHMSGSLLGI
                                                                                                                                                                                                                                                                                                                                                                                                                 VALFSKNSKELYFSILALWELGKELLFLNTHLTLAELTFQLKDAQVKTIIGAPE-----
                                       IFFFSLIRYDVTTGEFIRDPQGHCMATSPGEFGLLVAPVSQQSP--FLG--YAGGFELAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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23.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Streptococcus faecalis).
Lactobacillales; Enterococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 259; DB 1; 1
Pred. No. 4.9e-10;
1; Mismatches 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O-succinylbenzoate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       se; Complete proteome.
1BAD82BCB5C08F82 CRC64;
                                                                                                                                                                                                                                                                                                                                  -TQALLEEISFVDVQPMIKKQHSLSHQEFQQPSDLES
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(See http://www.isb-sib.ch/announce/
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  -IVDELGQEQPEKQVGEILLKGPNVVS
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GKLLKDVFRP-

-GDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGENVATTEVAEVFE

612

Search Job ti	Дb	δ	Дb	δ.	Db
Search completed: June 30, 2004, 17:33:53 Job time : 19 secs	459 HSFPQTASGKIAKHRENTE 477	673 ESLATTETFKQQKVRMANE 691	402 AITGIKAAAVVGEPDAQWGAVPVAYVI-SDQEITLAQIQDQCSRKLAKYKRPKRIYFC 458	613 ALDFLQEVNVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPPYARPRFLRLQ 672	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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